

AC005339

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502

5 F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

10 F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146

15 F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747

F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553

F-MAMMA1000862

20 F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906

25 F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336

30 F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283

35 F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

40 F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

45 F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117

50 F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308

F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643

55 F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001

F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

- 5 F-MAMMA1000975//Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458
- F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991
- 10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114
- F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406
- F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401
- 15 F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929
- F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567
- 20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701
- F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444
- 25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990
- F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903
- F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597
- 30 F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457
- F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125
- 35 F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169
- F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420
- F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733
- 40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749
- F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:334:69//AC006120
- F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155
- 45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087
- F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256
- F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019
- 50 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045
- F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637
- 55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825
- F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116



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F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//1.6e-84:406:82//S70011  
F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence//1.3e-14:182:76//AL022339  
5 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS//5.2e-87:714:78//Z71187  
F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence//0.00051:249:61//AQ055735  
F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence//2.2e-30:410:70//AC004518  
10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01//2.4e-13:87:100//AF086123  
F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds//9.3e-15:432:60//U31629  
F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence//6.8e-57:670:72//AC005696  
F-MAMMA1001191  
15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds//1.5e-117:759:84//U29156  
F-MAMMA1001202  
F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces//1.5e-161:764:98//AC005412  
F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence//5.1e-30:535:65//AC004099  
20 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//8.4e-182:860:98//AC005393  
F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence//7.7e-58:690:70//AC004875  
25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds//2.7e-07:624:58//M34398  
F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence//0.91:177:66//AC005726  
F-MAMMA1001244  
F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence//6.7e-09:502:58//U67616  
30 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence//5.0e-37:342:80//Z99495  
F-MAMMA1001259  
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//8.7e-40:659:64//AB014561  
35 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//4.9e-43:265:81//AC004453  
F-MAMMA1001271//Salmo salar DNA for a cryptic repeat//2.6e-06:311:63//AJ012206  
F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces//6.6e-70:327:83//AC004840  
40 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.0e-05:276:66//AC003035  
F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence//3.6e-98:199:98//AL022314  
45 F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence//4.7e-33:292:71//AQ030084  
F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence//1.6e-182:860:98//AC005703  
50 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence//1.9e-70:163:97//Z93244  
F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence//2.6e-19:379:68//AL031290  
55 F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE//4.5e-131:751:90//AL031390  
F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906  
 F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744  
 F-MAMMA1001346  
 5 F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086  
 F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826  
 F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS  
 10 and GSS, complete sequence.//1.6e-23 :209:75//AL022332  
 F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300  
 F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872  
 15 F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75 :424:93//AQ244585  
 F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049  
 F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400  
 20 F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684  
 F-MAMMA1001452//RPC11-48022.TJ RPC11 Homo sapiens genomic clone R-48O22, genomic survey sequence.//5.3e-87:423:98//AQ199294  
 25 F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543  
 F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783  
 F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486  
 30 F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366  
 F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714  
 35 F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378  
 F-MAMMA1001522  
 F-MAMMA1001547  
 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931  
 40 F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548  
 F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764  
 F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949  
 45 F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-66:405:90//AQ163791  
 F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626  
 F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685  
 50 F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630  
 F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833  
 F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412  
 55 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796  
 F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

- F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577
- 5 F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284  
F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491  
F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779
- 10 F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614  
F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118  
F-MAMMA1001683//Spermatogenesis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970
- 15 F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345  
F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228
- 20 F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845  
F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125  
F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687
- 25 F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913  
F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001  
F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//3.2e-16:194:75//AC006017
- 30 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998  
F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718
- 35 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065  
F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338  
F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865
- 40 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722
- 45 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514  
F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801  
F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801
- 50 F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991  
F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563  
F-MAMMA1001785  
F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129
- 55 F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

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F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262

F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128

F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031

F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930

10 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148

F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508

F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete sequence.//3.4e-45:312:85//AC006211

15 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042

F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620

F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390

20 F-MAMMA1001854

F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631

F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013

25 F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455

F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63h5, reverse read cpg63h5.rtl.//1.0:127:63//Z62129

F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

30 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465

F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

35 F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597

F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157

40 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656

F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986

45 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071

F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646

F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_O\_I, complete sequence.//1.5e-07:244:62//AC005224

50 F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803

55 F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227

F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//

AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCII1-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576  
 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:  
 67//AC003108  
 F-MAMMA1002292//B.garinii (strain Tls1) p83/100 gene (partial).//0.73:200:64//X81533  
 5 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
 1.6e-56:408:75//AC006023  
 F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258  
 F-MAMMA1002297  
 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:  
 10 525:61//AC004221  
 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey se-  
 quence.//1.2e-90:446:98//AQ053994  
 F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING  
 DRAFT SEQUENCE.//1.3e-35:329:78//AL031680  
 15 F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gene, complete cds.//0.0060:301:60//J05451  
 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syn-  
 drome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737  
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and  
 STS.//1.3e-09:741:58//Z86064  
 20 F-MAMMA1002317  
 F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//  
 AC005756  
 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:  
 617:70//AC004796  
 25 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//  
 U93871  
 F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING  
 DRAFT SEQUENCE.//1.6e-31:287:74//AL034402  
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//  
 30 AL022022  
 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases  
 1.41604.//2.1e-57:522:77//AJ011932  
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//  
 AC004129  
 35 F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORK-  
 ING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100  
 F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING  
 DRAFT SEQUENCE.//5.8e-17:326:70//Z98742  
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 40 1.1e-14:399:63//AC004825  
 F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING  
 DRAFT SEQUENCE.//3.7e-43:420:75//AL023879  
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153  
 45 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence.//5.3e-18:156:75//AC005831  
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome  
 4p16.3, contains EST.//4.9e-43:353:69//Z68885  
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs  
 50 and a GSS, complete sequence.//1.8e-22:282:74//AL008719  
 F-MAMMA1002362//Platymys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938  
 F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey se-  
 quence.//4.4e-10:85:92//AQ196889  
 F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey se-  
 55 quence.//2.7e-56:286:98//AQ284134  
 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey se-  
 quence.//5.5e-46:335:84//AQ043985  
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//

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AC004888  
 F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875  
 F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608  
 5 F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402  
 F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604  
 10 F-MAMMA1002428  
 F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023  
 F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479  
 15 F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229  
 F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005  
 F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556  
 20 F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671  
 F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077  
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460  
 25 F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913  
 F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477  
 F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359  
 30 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214  
 F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22 complete sequence.//1.9e-41:345:80//AC005696  
 F-MAMMA1002554  
 35 F-MAMMA1002556  
 F-MAMMA1002566  
 F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579  
 F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507  
 40 F-MAMMA1002585  
 F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019  
 F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548  
 45 F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958  
 F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220  
 F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861  
 50 F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486  
 F-MAMMA1002618  
 F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598  
 55 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449  
 F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660  
 F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING

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DRAFT SEQUENCE.//1.9e-171:819:98//AL031727  
 F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093  
 F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063  
 F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666  
 5 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//  
 AC002038  
 F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:  
 59//L41919  
 F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 10 nomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233  
 F-MAMMA1002662  
 F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//  
 AC005029  
 F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398  
 15 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987  
 F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING  
 DRAFT SEQUENCE.//6.2e-45:510:70//AL023585  
 F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 20 nomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214  
 F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//  
 AF018261  
 F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399  
 F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of  
 25 the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053  
 F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//  
 AC005030  
 F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey se-  
 quence.//1.4e-06:265:63//AQ061245  
 30 F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2  
 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene.  
 Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584  
 F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokerin exon, delta-  
 aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/  
 35 fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821  
 F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:  
 535:58//AE001368  
 F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:  
 97//AC005856  
 40 F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//2.7e-175:829:98//AC006055  
 F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
 pieces.//3.1e-31:372:75//AC004676  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902  
 45 F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636  
 F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey  
 sequence.//6.7e-13:155:76//B92153  
 F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey se-  
 quence.//9.7e-21:151:90//AQ028244  
 50 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene,  
 complete cds.//5.6e-105:179:99//U07561  
 F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, com-  
 plete sequence.//0.071:277:58//Z98546  
 F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 55 nomic clone Plate=3213 Col=16 Row=D; genomic survey sequence.//0.00018:219:63//AQ175845  
 F-MAMMA1002796  
 F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; com-  
 plete sequence.//6.9e-22:332:69//AC002404



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F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035  
F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529110, complete sequence.//1.0e-64:320:83//AC002553  
5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875  
F-MAMMA1002835  
F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462  
10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883  
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353  
F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616  
F-MAMMA1002858  
15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566  
F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863  
F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388  
F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518  
20 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027  
F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653  
F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814  
25 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906  
F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096  
30 F-MAMMA1002895//H.sapiens CpG island DNA genomic MseI fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616  
F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828  
F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402  
F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467  
35 F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623  
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598  
F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032  
40 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496  
F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366  
F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056  
45 F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272  
F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919  
F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:63//AL022098  
50 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871  
F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998  
55 F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601  
F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139  
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//  
 AC003694  
 5 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-  
 13:443:61//AC003661  
 F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271  
 F-MAMMA1003026  
 10 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//  
 0.0037:134:73//AC005214  
 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey se-  
 quence.//1.1e-07:66:100//B74936  
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//2.1e-19:220:76//AC004671  
 15 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, poly-  
 morphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257  
 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS,  
 complete sequence.//0.21:289:61//AL031321  
 20 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-  
 139:663:98//AF077952  
 F-MAMMA1003049  
 F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940  
 25 F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772  
 F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352  
 F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING  
 DRAFT SEQUENCE.//1.0:142:71//AL034371  
 30 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:  
 373:78//AC004796  
 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166  
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:  
 477:64//U72634  
 35 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:  
 85//AF071316  
 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199  
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:  
 676:58//U67916  
 40 F-MAMMA1003140  
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062  
 F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE.//7.3e-123:266:88//AL021579  
 F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
 DRAFT SEQUENCE.//1.6e-33:143:82//Z99716  
 45 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
 complete sequence.//0.50:216:61//Z95400  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886  
 F-NT2RM1000032  
 50 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-  
 135:565:84//U67060  
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590  
 F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155  
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671  
 55 F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING  
 DRAFT SEQUENCE.//1.0:257:59//AL031600  
 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520  
 F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594  
 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155  
 F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING  
 5 DRAFT SEQUENCE.//0.022:644:58//Z97630  
 F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884  
 F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335  
 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene en-  
 10 coding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959  
 F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890  
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155  
 F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey se-  
 quence.//1.1e-05:56:98//AQ261184  
 15 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009  
 F-NT2RM1000242  
 F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474  
 20 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complete sequence.//0.023:225:61//AC006070  
 F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:473:64//Z68336  
 F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940  
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:80//D50920  
 25 F-NT2RM1000271  
 F-NT2RM1000272  
 F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927  
 F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING  
 30 DRAFT SEQUENCE.//2.1e-96:170:100//Z93097  
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880  
 F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205  
 F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879  
 F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 35 nomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494  
 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253  
 F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821  
 F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302  
 40 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679  
 F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979  
 F-NT2RM1000399  
 F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737  
 45 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928  
 F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989  
 F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993  
 50 F-NT2RM1000553  
 F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542  
 F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873  
 F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 55 nomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737  
 F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078  
 F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

5 F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

10 F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

15 F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

20 F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

25 F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542

F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134

30 F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840

35 F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519c13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228

40 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

45 F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

50 F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

55 F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

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F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125  
F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245  
F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915  
F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391  
F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905  
F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263  
F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731  
F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757  
F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489  
F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964  
F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973  
F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678  
F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624  
F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755  
F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291  
F-NT2RM2000013//D.melanogaster DmrP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826  
F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863  
F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379  
F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418  
F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269  
F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905  
F-NT2RM2000101  
F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303  
F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224  
F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289  
F-NT2RM2000239//F. rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549  
F-nnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292  
F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162  
F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658  
F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934  
F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

- QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656  
 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864
- 5 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132  
 F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300  
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251
- 10 F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343  
 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514  
 F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274  
 F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973
- 15 F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430  
 F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204  
 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022  
 F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794
- 20 F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041  
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290  
 F-NT2RM2000502
- 25 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243  
 F-NT2RM2000522  
 F-NT2RM2000540  
 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466
- 30 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132  
 F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252  
 F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681
- 35 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391  
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987  
 F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466
- 40 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626  
 F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988  
 F-NT2RM2000609
- 45 F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776  
 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952  
 F-NT2RM2000624  
 2.9e-06:231:64//Z82061
- 50 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272  
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558  
 F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
- 55 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576  
 F-NT2RM2000669  
 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038  
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342  
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244  
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691  
 F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING  
 5 DRAFT SEQUENCE.//1.0e-78:723:76//AL021392  
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228  
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//  
 AC005017  
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046  
 10 F-NT2RM2000952  
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-  
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//  
 7.6e-41:239:76//AF109905  
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-  
 15 quence.//1.1e-11:298:66//AQ035862  
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855  
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//  
 AF071314  
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-  
 20 145:614:99//AC004873  
 F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//2.7e-95:461:99//AL034380  
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-  
 24:726:62//U52064  
 25 F-NT2RM2001141  
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the  
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-  
 ponent A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-  
 plete sequence.//0.98:300:62//AL022401  
 30 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 1.2e-147:741:96//AC005488  
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial  
 cds.//0.026:408:59//U66829  
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-  
 35 135:627:98//AC004987  
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700  
 F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514  
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150  
 F-NT2RM2001243  
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey  
 sequence.//0.0011:274:59//AQ276184  
 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169  
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-  
 quence.//4.6e-09:156:72//B57734  
 45 F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey se-  
 quence.//0.069:234:64//B84850  
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:  
 81//AC005919  
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118  
 50 F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING  
 DRAFT SEQUENCE.//3.7e-44:340:85//Z84465  
 F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514  
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//  
 55 U56429  
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//  
 AC004899  
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete

sequence.//4.0e-54:394:75//AC004033  
 F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//2.8e-169:789:99//AL033520  
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509  
 5 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:  
 83//AB000113  
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//  
 AC005624  
 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:  
 10 65//Z99708  
 F-NT2RM2001544  
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657  
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551  
 F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750  
 15 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902  
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667  
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455  
 nt].//2.3e-85:749:75//S66431  
 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630  
 20 F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//  
 AC004691  
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518  
 F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//  
 Z91020  
 25 F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey se-  
 quence.//1.3e-67:340:98//AQ060913  
 F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629  
 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-  
 153:807:93//AF023451  
 30 F-NT2RM2001659//nxbx0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nxbx0002J13f, genomic  
 survey sequence.//1.0:485:56//AQ051653  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//  
 3.7e-172:802:99//AF044195  
 F-NT2RM2001668  
 35 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing  
 Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147  
 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:  
 683:94//U21157  
 F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone R-51J16, genomic survey se-  
 40 quence.//1.0:394:58//AQ053677  
 F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//  
 AL021890  
 F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS  
 genes.//1.0:286:62//X52948  
 45 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey se-  
 quence.//3.2e-53:241:82//B59854  
 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//  
 M10668  
 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains  
 50 protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:  
 59//AL021920  
 F-NT2RM2001699//HS\_3195\_8B2\_DO1\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056  
 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//  
 55 Z95556  
 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered  
 pieces.//7.5e-42:335:81//AC004469  
 F-NT2RM2001716



- F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290
- F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123
- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931
- 5 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598
- F-NT2RM2001743
- F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117
- F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629
- F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- 10 nomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116
- F-NT2RM2001782
- F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053
- 15 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
- F-NT2RM2001797//HS\_3045\_AT\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- nomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456
- F-NT2RM2001800
- 20 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195
- F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126
- F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey se-
- 25 quence.//3.3e-16:109:95//B89870
- F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759
- F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//
- 30 AC002347
- F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
- nomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285
- F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the
- 35 gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177
- F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chro-
- 40 mosome X.//0.0029:500:59//Z68328
- F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610
- F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720
- F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931
- F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818
- F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028
- 45 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
- F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
- F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825
- 50 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
- F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
- F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955
- F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding
- 55 carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
- F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
- F-NT2RM2002014
- F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//

1.5e-89:822:74//U00932  
 F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132  
 F-NT2RM2002055  
 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//  
 5 AF073936  
 F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//4.6e-160:771:98//AL034380  
 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840  
 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//  
 10 2.4e-143:684:98//AF030435  
 F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete  
 cds.//7.0e-27:330:73//U13152  
 F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121  
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:  
 15 92//AF084928  
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936  
 F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-  
 13:337:62//AC004423  
 F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:  
 20 801:70//X58826  
 F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429  
 F-NT2RM4000030//H.sapiens CpG island DNA genomic Mse1 fragment, clone 56h10, forward read  
 cpg56h10.ft1a.//9.3e-22:127:100//Z55685  
 F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059  
 25 F-NT2RM4000061  
 F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829  
 F-NT2RM4000086  
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//  
 4.2e-23:345:69//AF060865  
 30 F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101  
 F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey se-  
 quence.//3.0e-09:88:90//AQ000070  
 F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586:60//X67336  
 F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:  
 35 90//D12646  
 F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157  
 F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:  
 60//AF051726  
 40 F-NT2RM4000197  
 F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
 DRAFT SEQUENCE.//0.67:461:60//AL031667  
 F-NT2RM4000200  
 F-NT2RM4000202//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34c2, forward read cpg34c2.ft1a.//  
 45 1.7e-27:190:90//Z65361  
 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255  
 F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:  
 62//J03852  
 F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
 50 4.6e-102:233:94//AC005383  
 F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430  
 F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey  
 sequence.//5.5e-08:422:62//B86757  
 F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete  
 55 sequence.//0.98:207:60//AC005855  
 F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-  
 cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689  
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

M99438

F-NT2RM4000324

F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085

5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430

F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449

10 F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542

F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217

F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485

15 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//1.5e-37:295:82//AC005921

20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476

F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111

F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952

25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908

F-NT2RM4000511

F-NT2RM4000514

30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113

F-NT2RM4000520

F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297

35 F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706

F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125

40 F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390

45 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303

50 F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

F-NT2RM4000717

55 F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303

F-NT2RM4000741

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F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593  
F-NT2RM4000764  
F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790  
5 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920  
F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206  
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//  
10 AC005306  
F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663  
F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988  
F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451  
15 F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109  
F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406  
F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373  
20 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940  
F-NT2RM4000852  
F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//3.4e-29:229:83//AC003957  
25 F-NT2RM4000887  
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004  
F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929  
30 F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735  
F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245  
F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651  
35 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272  
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539  
F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276  
F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858  
40 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629  
F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479  
F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776  
45 F-NT2RM4001116  
F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593  
F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249  
50 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706  
F-NT2RM4001160  
F-NT2RM4001187  
F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378  
55 F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933  
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828  
F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381  
 F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884  
 F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 5 nomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676  
 F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163  
 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973  
 10 F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002  
 F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016  
 F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127  
 F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORK-  
 15 ING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388  
 F-NT2RM4001347  
 F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786  
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799  
 20 F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393  
 F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SE-  
 QUENCE.//0.027:336:58//AP000023  
 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, com-  
 25 plete cds.//5.9e-124:783:85//AF020526  
 F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183  
 F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563  
 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-  
 30 47:623:69//AC004226  
 F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and iso-  
 leucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901  
 35 F-NT2RM4001454  
 F-NT2RM4001455  
 F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367  
 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585  
 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
 40 DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688  
 F-NT2RM4001522//Human HepG2 3' region Mbol cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274  
 F-NT2RM4001557  
 F-NT2RM4001565  
 F-NT2RM4001566  
 45 F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720  
 F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//  
 AF071317  
 F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942  
 50 F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered  
 pieces.//0.34:388:59//AC002355  
 F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750  
 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334  
 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//  
 55 D90910  
 F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196  
 F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

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F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320  
F-NT2RM4001666  
F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699  
F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
5 DRAFT SEQUENCE.//1.9e-151:564:97//AL031447  
F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957  
F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
complete sequence.//1.2e-91:488:94//AL034430  
F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312  
10 F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123  
F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING  
DRAFT SEQUENCE.//2.3e-49:320:89//AL031709  
F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Li-  
brary) complete sequence.//6.3e-64:379:76//AC005831  
15 F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868  
F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270  
F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017  
F-NT2RM4001810  
F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//  
20 AC005036  
F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
4.4e-34:195:95//M37712  
F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046  
F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:  
25 72//U28687  
F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete se-  
quence.//1.0:406:60//AC000076  
F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2,  
complete cds.//1.6e-131:831:86//AF033275  
30 F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513  
F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855  
F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433  
F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711  
35 F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//  
Z88651  
F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey se-  
quence.//0.0025:61:88//AQ060809  
F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335  
40 F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732  
F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence.//  
4.9e-10:269:63//AB005248  
F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:  
45 100//AC005207  
F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162  
F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046  
F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
50 non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868  
F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330  
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341  
F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:  
502:60//Z82253  
55 F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-  
quence.//2.6e-33:177:99//AQ051701  
F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//  
AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344  
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712  
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882  
 5 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283  
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540  
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122  
 10 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267  
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783  
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216  
 15 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569  
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789  
 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646  
 F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RM4002140  
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152  
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940  
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763  
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540  
 30 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636  
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430  
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684  
 35 F-NT2RM4002213  
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160  
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448  
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959  
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779  
 F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653  
 45 F-NT2RM4002281  
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515  
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457  
 50 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881  
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-gene similar to GPIISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822  
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865  
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549  
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

5 F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

10 F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

15 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255

20 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484

25 F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

30 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402

35 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

40 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

45 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2.//2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555

50 F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

55 F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//E08546

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//



1.9e-20:431:64//AC006030  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535  
 F-NT2RP1000191  
 5 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496  
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508:69//AC004373  
 F-NT2RP1000259  
 10 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383  
 F-NT2RP1000324//RPC11-81O21.TJ RPC11 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.8e-29:182:92//AQ285136  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551  
 15 F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525  
 F-NT2RP1000348//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rt1c.//1.7e-09:71:100//Z56610  
 F-NT2RP1000357  
 20 F-NT2RP1000358 5.7e-16:403:61//AC005456  
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594  
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558  
 25 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159  
 F-NT2RP1000416  
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//L40178  
 F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305  
 30 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047  
 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//4.9e-80:196:95//AC002985  
 35 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634  
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neurectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:562:88//Z99297  
 40 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686  
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648  
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895  
 45 F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.//1.2e-08:331:63//U26264  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418  
 F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128  
 50 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770  
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419  
 55 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989  
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

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F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907  
F-NT2RP1000695  
F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536  
5 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932  
F-NT2RP1000730  
F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742  
10 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434  
F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344  
F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442  
15 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840  
F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213  
F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244  
20 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837  
F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020  
25 F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398  
F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629  
30 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812  
F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840  
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094  
35 F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199  
F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761  
F-NT2RP1000916  
F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362  
40 F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269  
F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483  
F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950  
45 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068  
F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263  
F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981//M60858  
F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126  
50 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435  
F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925  
F-NT2RP1001013//HS\_3068\_B1\_809\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667  
55 F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711  
F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073\_F\_15, complete sequence.//1.3e-134:241:99//AC004686

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F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267

5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938

F-NT2RP1001113

F-NT2RP1001173

F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681/U79139

10 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508

F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128 : 99//AC002036

15 F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63/L44140

F-NT2RP1001294

20 F-NT2RP1001302

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

F-NT2RP1001311//RPC111-67O14.TK RPC111 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291

F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

25 F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

30 F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424

35 F-NT2RP1001432

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

40 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375

F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316

F-NT2RP1001494

F-NT2RP10015431//Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280

45 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840

F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP100T616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081

F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856

55 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390

F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//

AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290

5 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092

F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610

10 F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037

15 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338

20 F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363

F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961

25 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356

F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365

30 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

35 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924

40 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

45 F-NT2RP2000195//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

50 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632

55 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401

F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:

87//AC004066  
 F-NT2RP2000248  
 F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORK-  
 ING DRAFT SEQUENCE.//0.0078:286:60//AL021388  
 5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey se-  
 quence.//5.7e-82:416:97//AQ059184  
 F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//4.5e-  
 29:310:73//AC006116  
 F-NT2RP2000274  
 10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and - 9.//4.6e-69:744:70//  
 M27877  
 15 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530  
 F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082  
 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the  
 HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE  
 pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
 20 complete sequence.//8.3e-144:731:95//AL022398  
 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
 complete sequence.//1.9e-102:555:90//AL034430  
 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//  
 M25757  
 25 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.6e-129:627:  
 97//U83981  
 F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 30 nomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835  
 F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like  
 pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010  
 F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093  
 35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:  
 96//AF102265  
 F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey se-  
 quence.//0.96:61:78//AQ276878  
 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//  
 40 AC004691  
 F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747  
 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:  
 73//Z92844  
 F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//  
 45 AC005229  
 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:  
 64//AL026277  
 F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//  
 0.19:72:81//U21671  
 50 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING  
 DRAFT SEQUENCE.//5.0e-115:570:96//AL022318  
 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543  
 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//  
 AC005321  
 55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514  
 F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486  
 F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386  
 F-NT2RP2000668  
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 5 4.3e-22:433:62//AC004916  
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913  
 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122  
 10 F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540  
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965  
 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293  
 15 F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887  
 F-NT2RP2000809  
 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698  
 20 F-NT2RP2000814  
 F-NT2RP2000816  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292  
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479  
 25 F-NT2RP2000845  
 F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284  
 F-NT2RP2000892  
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266  
 30 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014  
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298  
 35 F-NT2RP2000965  
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393  
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//1.6e-72:498:82//AC005277  
 40 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394  
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167  
 F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224  
 45 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957  
 F-NT2RP2001065  
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561  
 50 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423  
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063  
 F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596  
 55 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072  
 F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

- F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076
- F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); trans-located to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178
- F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949
- F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306
- F-NT2RP2001196
- F-NT2RP2001218
- F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893
- F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760
- F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177
- F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353
- F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430
- F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455
- F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594
- F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967
- F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783
- F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539
- F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147
- F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305
- F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721
- F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371
- F-NT2RP2001392//S.pristinaespiralis snbC gene & amp; snbDE gene.//0.019:267:59//Y11548
- F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242
- F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219
- F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759
- F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454
- F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065
- F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702
- F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350
- F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275
- F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931
- F-NT2RP2001450
- F-NT2RP2001467
- F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561
- F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355
- F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494
- F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596
- F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586
- F-NT2RP2001560
- F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430

5 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784

10 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354

15 F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699

20 F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

25 F-NT2RP2001721//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697

30 F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378

35 F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D\_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309

40 F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161

45 F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic Mse1 fragment, clone 97f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125

50 F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033

55 F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442

F-NT2RP2001969//H.sapiens CpG island DNA genomic Mse1 fragment, clone 152a8, reverse read cpg152a8.rt1a.//1.0e-20:123:99//Z59378

F-NT2RP2001976



F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117  
 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299  
 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:  
 5 65//AC005895  
 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-  
 12:160:79//AC004825  
 F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029  
 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete  
 10 sequence.//2.2e-86:722:77//AC004552  
 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon  
 of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375  
 F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301  
 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//  
 15 U87306  
 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=add-  
 ucin beta subunit 63 kda isoform/membrane skeleton protein (alternatively spliced, exon 10 to 13 region) [human,  
 Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183  
 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//  
 20 0.14:191:64//AQ249805  
 F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509  
 F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpG10h8.ft1a.//  
 25 2.4e-29:178:94//Z58857  
 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-  
 quence.//2.5e-32:202:92//B64468  
 F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//  
 M25874  
 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923  
 F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169  
 F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey se-  
 quence.//2.8e-18:109:100//AQ201833  
 F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complete cds.//2.7e-36:363:78//U09215  
 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-  
 82:477:89//AF032872  
 F-NT2RP2002208  
 F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 40 DRAFT SEQUENCE.//1.0:378:58//AL034557  
 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308  
 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998  
 F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418  
 F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING  
 DRAFT SEQUENCE.//9.7e-67:340:89//AL033527  
 F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey se-  
 quence.//2.9e-18:79:93//AQ268098  
 F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
 50 DRAFT SEQUENCE.//1.0:290:60//AL031033  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//  
 AF069532  
 F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673  
 F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594  
 F-NT2RP2002333  
 F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//

Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

5 F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742

F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682

F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169

10 F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045

F-NT2RP2002475

15 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//7.2e-18:134:90//AC006213

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334

F-NT2RP2002520

20 F-NT2RP2002537

F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127

F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317

25 F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304

F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155

F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181

F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310

30 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397

35 F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572

40 F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107

F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388

F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861

F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016

45 F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433

50 F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837

55 F-NT2RP2002800

F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

# EP 1 074 617 A2

TRB-4.//0.85:93:68//M18845  
 F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344  
 F-NT2RP2002880  
 5 F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey se-  
 quence.//0.11:53:90//AQ019792  
 F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//  
 AF038392  
 10 F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey sequence.//3.9e-06:66:83//  
 AL017246  
 F-NT2RP2002939  
 F-NT2RP2002954  
 F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//  
 15 U62483  
 F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey se-  
 quence.//4.6e-96:476:97//AQ057233  
 F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230  
 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//  
 20 AF059569  
 F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:  
 293:67//AC000958  
 F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//  
 AF025424  
 25 F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 2.3e-46:474:76//AC004765  
 F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//4.2e-23:202:  
 82//AC005703  
 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//  
 30 Z83822  
 F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786  
 F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362  
 F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 35 nomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797  
 F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//  
 AF079765  
 F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//  
 AC005329  
 40 F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915  
 F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey se-  
 quence.//5.0e-78:393:97//AQ012976  
 F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//  
 Z84716  
 45 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025  
 F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey se-  
 quence.//0.0025:156:67//AQ262657  
 F-NT2RP2003164  
 F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-  
 50 chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-  
 43:334:79//U91328  
 F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:  
 346:62//U50040  
 F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING  
 55 DRAFT SEQUENCE.//1.7e-108:511:90//AL031597  
 F-NT2RP2003206  
 F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794  
 F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:

86//AF023657  
 F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447  
 F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107  
 5 F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481  
 F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833  
 10 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525  
 F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286  
 F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024  
 15 F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973  
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572  
 F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722  
 20 F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666  
 F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374  
 F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288  
 F-NT2RP2003339  
 25 F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559  
 F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510  
 F-NT2RP2003391  
 F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356  
 30 F-NT2RP2003394  
 F-NT2RP2003401  
 F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630  
 F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023  
 35 F-NT2RP2003446  
 F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272  
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770  
 40 F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977  
 F-NT2RP2003499 2.1e-08:408:61//AB000826  
 F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236  
 45 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460  
 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702  
 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977  
 50 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899  
 F-NT2RP2003543  
 F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.r1a.//1.1e-20:122:99//Z56144  
 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551  
 55 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931  
 F-NT2RP2003581  
 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//J1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:98//AF030233  
 F-NT2RP2003629  
 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215  
 5 F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081  
 F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684  
 10 F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807  
 F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803  
 F-NT2RP2003704//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2a9, reverse read cpg2a9.rt1e.//3.8e-17:170:84//Z60615  
 15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097  
 F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895  
 F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973  
 20 F-NT2RP2003727//RPC11-77I19.TV RPC11 Homo sapiens genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303  
 F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951  
 F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964  
 25 F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987  
 F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275  
 F-NT2RP2003769  
 F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:98//AC004771  
 30 F-NT2RP2003777  
 F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011  
 F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761  
 35 F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491  
 F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167  
 F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467  
 40 F-NT2RP2003859  
 F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375  
 F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722  
 45 F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828  
 F-NT2RP2003952  
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458  
 50 F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282  
 55

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347  
 F-NT2RP2003984  
 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382  
 5 F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681  
 F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580  
 F-NT2RP2004014  
 10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555  
 15 F-NT2RP2004081  
 F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694  
 F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993  
 20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645  
 F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493  
 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140  
 25 F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235  
 F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816  
 F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093  
 30 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998  
 F-NT2RP2004196  
 F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676  
 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813  
 35 F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756  
 F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718  
 F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006  
 40 F-NT2RP2004242  
 F-NT2RP2004245  
 F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446  
 F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781  
 45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416  
 F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423  
 F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519  
 50 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650  
 F-NT2RP2004364  
 F-NT2RP2004365  
 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864  
 55 F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969  
F-NT2RP2004392  
5 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164  
F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799  
F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441  
10 F-NT2RP2004412//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369  
F-NT2RP2004425  
F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530  
F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388  
F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591  
15 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556  
F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890  
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163  
F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555  
20 F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100  
F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755  
F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908  
25 F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020  
F-NT2RP2004600  
F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176  
30 F-NT2RP2004614  
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291  
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929  
F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805  
35 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312  
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525  
F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714  
40 F-NT2RP2004710//HS\_3185\_82\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885  
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947  
F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022  
45 F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210  
F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636  
F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398  
50 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353:84//U56252  
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802  
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179  
55 F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519  
F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence.//0.96:183:64//AL025645

F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//4.8e-142:710:96//AC004383  
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144  
 F-NT2RP2004936  
 5 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183  
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-  
 59:339:79//U56732  
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-  
 10 chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-  
 19:187:72//U91328  
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551  
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029  
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:  
 273:61//B12642  
 15 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375  
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200  
 20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141  
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//  
 AC004849  
 F-NT2RP2005020  
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 25 3.0e-43:98:93//AC000380  
 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464  
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454  
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//  
 30 AC005696  
 F-NT2RP2005108  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//  
 X98743  
 35 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//  
 0.00024:547:59//AJ223012  
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
 quence.//0.95:191:62//AC004527  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583  
 40 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226  
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read  
 cpg132g6.ft1a.//1.1e-13:93:97//Z59162  
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070  
 45 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509  
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:  
 60//U80808  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//  
 AC005189  
 50 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536  
 F-NT2RP2005254  
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513  
 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666  
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335  
 55 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//  
 AF060219  
 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590  
 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-



nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701  
 5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138  
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844  
 10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247  
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358  
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184  
 F-NT2RP2005407  
 15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346  
 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548  
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865  
 20 F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647  
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679  
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-18:152:75//AC006116  
 25 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276  
 30 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130  
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030  
 35 F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847  
 F-NT2RP2005495  
 F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097  
 40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931  
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183:63//AC005880  
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695  
 45 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307  
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449  
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963  
 50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734  
 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723  
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529  
 55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016  
 F-NT2RP2005600//H.sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.rt1a.//0.32:134:63//Z57359  
 F-NT2RP2005605

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F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085  
F-NT2RP2005622  
F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556  
5 F-NT2RP2005637//NATI (NATI\*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829  
F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980  
F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763  
F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493  
10 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626  
F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605  
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814  
F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405  
15 F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836  
F-NT2RP2005694  
F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183  
20 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342  
F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603  
F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367  
F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528  
25 F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627  
F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017  
F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270  
30 F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342  
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868  
F-NT2RP2005753//Homo sapiens l-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516  
35 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853  
F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849  
F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836  
F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336  
40 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853  
F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423  
F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579  
45 F-NT2RP2005812  
F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103  
F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086  
F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873  
F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490  
50 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564  
F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553  
55 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//AL027276  
F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

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F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316  
F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpg15b5.rt1a.//0.0026:66:84//Z54729  
5 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241  
F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840  
F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770  
F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207  
10 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553  
F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912  
F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495  
15 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861  
F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047  
F-NT2RP2006071  
F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207  
20 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073  
F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602  
F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//11.2e-62:655:71//AC000378  
25 F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405  
F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063  
F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587  
30 F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554  
F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232  
F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057  
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484  
35 F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480  
F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055  
F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615  
40 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630  
F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257  
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262  
F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851  
45 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973  
F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532  
F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893  
50 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514  
F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590  
55 F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727  
F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441  
 F-NT2RP2006454//Sequence 8 from Patent WO9517522.//2.9e-06:180:66//A45338  
 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266  
 5 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201:66//U50149  
 F-NT2RP2006472  
 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism,  
 10 complete sequence.//8.8e-10:273:66//Z93929  
 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966  
 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:  
 15 503:63//M20855  
 F-NT2RP2006573//Mollusca contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315  
 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537  
 F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571  
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//  
 20 AJ011972  
 F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320  
 F-NT2RP3000047  
 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.0e-67:626:74//  
 25 M27877  
 F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227  
 F-NT2RP3000068  
 F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746  
 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING  
 30 DRAFT SEQUENCE.//1.9e-44:297:79//AL021391  
 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536  
 F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237  
 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete  
 35 cds.//0.92:185:64//L29260  
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189  
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164  
 40 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884  
 F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583  
 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063  
 45 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716  
 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569  
 50 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972  
 F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213  
 F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174:88//AF065393  
 F-NT2RP3000255  
 55 F-NT2RP3000267  
 F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853  
 F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932

F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107

F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090

5 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533

F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181

F-NT2RP3000348

10 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393

F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757

F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743

15 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966

F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318

F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185

F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, complete sequence.//7.9e-53:817:68//AC006083

20 F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471

25 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488

F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420

30 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

35 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667

F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

40 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

F-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

45 F-NT2RP3000562

F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

50 F-NT2RP3000584

F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868

55 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305

F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

- F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
- F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
- 5 F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
- F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
- F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete
- 10 sequence.//0.078:393:58//AL031313
- F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363
- F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
- F-NT2RP3000661
- 15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to *C. elegans* C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
- 20 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
- F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
- F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
- F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
- 25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655
- F-NT2RP3000753
- F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
- F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252
- 30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
- F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009
- 35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
- F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
- 40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
- F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
- F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E; ELAM-1 Endothelial Leukocyte
- 45 Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast. plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
- 50 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
- F-NT2RP3000865
- F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
- 55 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
- F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007
- F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//

AF021340  
 F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505:99//M27223  
 F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517  
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 5 3.2e-97:585:88//AF015264  
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:  
 89//U91326  
 F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335  
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 10 Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529  
 F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.rt1a./  
 15.9e-27:150:99//Z60925  
 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:  
 610:57//AC006039  
 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-  
 15 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653  
 F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//  
 AF060219  
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325  
 F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey se-  
 20 quence.//3.4e-37:222:93//AQ021278  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969  
 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma  
 25 (polg) gene, complete sequence.//2.7e-116:186:99//AC005317  
 F-NT2RP3001111  
 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chro-  
 mosome X.//2.4e-05:702:58//Z68871  
 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//  
 30 AC005189  
 F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581  
 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 35 complete sequence.//1.4e-121:598:97//AL031864  
 F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367  
 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:  
 64//Z49078  
 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//  
 40 AF027735  
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305  
 F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey se-  
 quence.//2.1e-15:106:96//B48859  
 F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 45 DRAFT SEQUENCE.//2.0e-159:418:95//AL034379  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266  
 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, com-  
 plete sequence.//1.1e-69:207:97//AL034351  
 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 50 DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507  
 F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-  
 05:561:56//AC004845  
 F-NT2RP3001221  
 F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619  
 55 F-NT2RP3001236  
 F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396  
 F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey se-  
 quence.//8.5e-70:337:100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430  
 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269  
 F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513  
 5 F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101  
 F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561  
 10 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457  
 F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465  
 F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 15 DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709  
 F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966  
 F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935  
 20 F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105  
 F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052  
 F-NT2RP3001356  
 F-NT2RP3001374  
 25 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628  
 F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332  
 F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198  
 30 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296  
 F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046  
 F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521  
 35 F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031  
 F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327  
 F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 40 DRAFT SEQUENCE.//2.9e-89:138:98//AL031447  
 F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997  
 F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668  
 45 F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619  
 F-NT2RP3001447  
 F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B  
 50 and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta.1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 55 complete sequence.//2.1e-105:223:99//AL031282  
 F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065



F-NT2RP3001457  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//  
 AF072836  
 5 F-NT2RP3001490  
 F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//  
 8.5e-171:804:98//AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:  
 10 91//U36499  
 F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete  
 cds.//2.1e-14:517:59//D87916  
 F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:  
 63//AF078176  
 15 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//  
 4.3e-17:332:67//M83196  
 F-NT2RP3001580//RPCI11 Homo sapiens genomic clone R-91E19, genomic survey se-  
 quence.//4.2e-15:110:91//AQ281332  
 F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104  
 20 F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey se-  
 quence.//8.7e-108:517:98//AQ237629  
 F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete  
 sequence.//1.0e-09:257:65//AC004674  
 F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane mo-  
 25 nooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//  
 M90050  
 F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger  
 protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,  
 STS, GSS, complete sequence.//1.8e-42:278:79//AL021808  
 30 F-NT2RP3001629  
 F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978  
 F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449  
 35 F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-  
 38:542:66//U49793  
 F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250  
 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORK-  
 40 ING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358  
 F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860  
 F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//  
 2.1e-37:512:70//AF059273  
 45 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-  
 quence.//2.8e-19:123:95//AQ012480  
 F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962  
 F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse read cpg4g7.rt1d.//  
 1.3e-17:113:97//Z61312  
 50 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642  
 F-NT2RP3001716  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:  
 565:97//AF054177  
 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:  
 88//AF008554  
 55 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918  
 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete se-  
 quence.//6.5e-07:178:69//AC000097

- F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311
- F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381
- F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888
- 5 F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644
- F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928
- F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262
- F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING-IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284
- 10 F-NT2RP3001819//S.glaucens genes strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides.//0.084:526:58//X89010
- F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433
- 15 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505
- F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknx1) mRNA, complete cds.//2.7e-39:575:67//AF061270
- F-NT2RP3001857//M.musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434
- 20 F-NT2RP3001896
- F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733
- F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:56//Z73969
- F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557
- 25 F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651
- F-NT2RP3001931
- F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475
- 30 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575
- F-NT2RP3001944
- F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
- 35 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694
- F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822
- 40 F-NT2RP3002004//Sequence.3 from patent US 5798245.//1.6e-26:104:100//AR025386
- F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
- F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
- 45 F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493
- F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
- F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841
- 50 F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
- F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
- F-NT2RP3002062
- F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272
- 55 F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
- F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-

- plete sequence.//9.6e-66:562:77//AC006210  
 F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040  
 F-NT2RP3002108  
 5 F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020  
 F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370  
 F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING  
 10 DRAFT SEQUENCE.//1.3e-63:380:91//AL031710  
 F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742  
 F-NT2RP3002163  
 F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061  
 15 F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//0.090:394:59//AC006121  
 F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219  
 F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808  
 20 F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321  
 F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880  
 25 F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321  
 F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004  
 30 F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898  
 F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810  
 F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 35 DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504  
 F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862  
 F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068  
 40 F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331  
 45 F-NT2RP3002399  
 F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578  
 F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927  
 50 F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068  
 F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272  
 55 F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821  
 F-NT2RP3002566//Streptomyces viridificans sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418  
 F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.6e-13:199:76//

AC004617  
 F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804  
 F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic  
 survey sequence.//2.0e-22:140:95//B68331  
 5 F-NT2RP3002603  
 F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050  
 F-NT2RP3002631  
 F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469  
 F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205  
 10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//  
 AC004946  
 F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//  
 AC006129  
 F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704  
 15 F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507  
 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey  
 sequence.//2.5e-25:173:91//B51656  
 F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577  
 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey se-  
 20 quence.//0.0012:55:92//AQ263530  
 F-NT2RP3002713  
 F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594  
 F-NT2RP3002770  
 F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short var-  
 25 iant, partial cds.//0.78:515:57//AF029325  
 F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene  
 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribos-  
 omal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete  
 sequence.//1.9e-21:167:79//AL022718  
 30 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//  
 AC005549  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715  
 F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601  
 F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430  
 35 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895  
 F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE,  
 100 unordered pieces.//7.9e-12:160:78//AC006087  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314  
 F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey  
 40 sequence.//2.3e-13:442:61//B88815  
 F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500  
 F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:  
 793:98//AC005754  
 F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024  
 45 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666  
 F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820  
 F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505  
 F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644  
 50 F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708  
 F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,  
 G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:  
 197:79//AF109905  
 55 F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete  
 sequence.//1.6e-08:809:58//AL010153  
 F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//  
 U78090

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1)//1.4e-12:633:59//X16609  
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410  
 F-NT2RP3003071//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read  
 cpg13d12.r1c.//6.8e-15:95:100//Z64565  
 5 F-NT2RP3003078  
 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315  
 F-NT2RP3003121  
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//  
 AC004510  
 10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//  
 D12646  
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//  
 U17995  
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639  
 15 F-NT2RP3003150  
 F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489  
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete  
 cds.//8.6e-06:228:65//AF064868  
 20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933  
 F-NT2RP3003197  
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 4.1e-48:640:67//AF015264  
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059  
 25 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799  
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:  
 776:74//U20286  
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064  
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460  
 30 F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200  
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153  
 F-NT2RP3003278//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//  
 4.0e-27:174:93//Z60555  
 35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983  
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:  
 71//AF004162  
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//  
 D85610  
 40 F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213  
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
 quence.//1.0:191:62//AC004527  
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107  
 F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200  
 45 F-NT2RP3003330  
 F-NT2RP3003344  
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:  
 84//AC005284  
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a  
 50 BAC end-sequence (GSS).//0.047:404:60//AL021069  
 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
 8.3e-122:632:96//AC005519  
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-  
 dered pieces.//0.0036:127:74//AC000360  
 55 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874  
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:  
 63//U90653

F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317  
 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173  
 5 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268  
 10 F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124  
 F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347  
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234  
 15 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049  
 F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985  
 20 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798  
 F-NT2RP3003572  
 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632  
 25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387  
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235  
 F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600  
 30 F-NT2RP3003656  
 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271  
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096  
 35 F-NT2RP3003672  
 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811  
 F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993  
 40 F-NT2RP3003701  
 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975  
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300  
 45 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785  
 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326  
 50 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458  
 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031  
 55 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321  
 F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801  
 F-NT2RP3003819

F-NT2RP3003825  
 F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626  
 F-NT2RP3003831//RPC11-50N15.TJ RPC11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633  
 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611  
 F-NT2RP3003842//RPC11-44E5.TJ RPC11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884  
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268  
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343  
 10 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181  
 F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554  
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358  
 15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504  
 F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661  
 F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837  
 20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692  
 F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726  
 F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400  
 25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317  
 F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939  
 30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089  
 F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433  
 F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038  
 35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973  
 F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560  
 F-NT2RP3004145  
 F-NT2RP3004148  
 40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900  
 F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102:82//X80434  
 F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374  
 F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009  
 45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052  
 F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084  
 F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181  
 F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385  
 50 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353  
 F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967  
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982  
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871  
 55 F-NT2RP3004332  
 F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908  
 F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877  
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete se-  
 quence.//5.1e-49:480:75//AC004025  
 5 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-  
 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249  
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678  
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206  
 F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey se-  
 10 quence.//8.8e-19:180:82//AQ052326  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917  
 F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458  
 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read  
 15 cpg81a11.r1a.//7.0e-25:148:96//Z56029  
 F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//  
 1.6e-20:143:92//AQ052792  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925  
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//  
 20 U47024  
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851  
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
 4.0e-67:265:84//AC006023  
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 25 complete sequence.//1.2e-55:415:78//AC004673  
 F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260  
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//  
 AC005328  
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574  
 30 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532  
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126  
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:  
 64//AF031955  
 35 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey se-  
 quence.//5.3e-15:138:84//AQ280780  
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//  
 AF026445  
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946  
 40 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266  
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-  
 14:360:65//AC004977  
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:  
 73//AF005355  
 45 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160  
 nt].//0.046:437:57//S69350  
 F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING  
 DRAFT SEQUENCE.//1.9e-05:625:59//Z98882  
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//1.5e-155:844:92//  
 50 AC006121  
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//  
 0.012:417:59//AB012242  
 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//  
 AC005035  
 55 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761  
 F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449  
 F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558



- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538  
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952  
 5 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776  
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681  
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088  
 F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551  
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210  
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600  
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300  
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261  
 F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504  
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470  
 20 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092  
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515  
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481  
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322  
 F-NT2RP4000323  
 30 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281  
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195  
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272  
 35 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536  
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850  
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116  
 40 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966  
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086  
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101  
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194  
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183  
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982  
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499  
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483  
 F-NT2RP4000481  
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125  
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904  
 F-NT2RP4000515  
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

- F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840  
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720
- 5 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498  
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386  
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443  
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465
- 10 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580  
 F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730
- 15 F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333  
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335  
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904
- 20 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852  
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149  
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
- 25 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301  
 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence.//1.1e-24:161:93//B57903  
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
- 30 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
- 35 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420  
 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216  
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
- 40 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367  
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616  
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
- 45 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901  
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
- 50 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975  
 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
- 55 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688  
 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519  
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657

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F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence.//6.5e-31:317:79//AQ015742  
F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942  
F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823  
5 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911  
F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358  
F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424  
10 F-NT2RP4001004  
F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176  
F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140  
15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086  
F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170  
F-NT2RP4001057  
F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469  
20 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124  
F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018  
F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372  
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164  
F-NT2RP4001095  
25 F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402  
F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629  
F-NT2RP4001122  
F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668  
30 F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969  
F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079  
F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095  
35 F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067  
F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952  
40 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476  
F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494  
F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rscI9) mRNA, partial cds.//0.032:453:58//U82511  
45 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358  
F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877  
F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251  
50 F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657  
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569  
F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081  
55 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061  
F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854  
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728  
 5 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250  
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119  
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870  
 10 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725  
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918  
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011  
 15 F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428  
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107  
 F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701  
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609  
 20 F-NT2RP4001375  
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153:88//AC005722  
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691  
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957  
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326  
 30 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884  
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523  
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612  
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693  
 35 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513  
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308  
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086  
 40 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663  
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335:60//AL032684  
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806  
 45 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290  
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989  
 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885  
 50 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987  
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:86//AJ223830  
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663:59//X74219  
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364  
 55 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333  
 F-NT2RP4001634  
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

- clone cSRL-161FI, genomic survey sequence.//4.9e-12:144:76//B02870  
 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092  
 F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793  
 5 F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362  
 F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING  
 DRAFT SEQUENCE.//2.7e-45:351:84//AL031431  
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//  
 U96629  
 10 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-  
 13:402:63//AC004296  
 F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey  
 sequence.//0.88:177:67//AQ029840  
 F-NT2RP4001739  
 15 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:  
 192:98//Z96232  
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316  
 F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:74//AC005678  
 F-NT2RP4001803  
 20 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//  
 AF054841  
 F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2  
 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete  
 sequence.//2.1e-08:601:59//Z98743  
 25 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888  
 F-NT2RP4001841  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572  
 F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691  
 30 F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//  
 AC005014  
 F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:  
 35 354:61//B26193  
 F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//  
 0.031 :409:60//AB011413  
 F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677  
 40 F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046  
 F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185  
 F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-  
 tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,  
 45 subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,  
 complete sequence.//2.1e-18:421:65//AL022577  
 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey se-  
 quence.//0.030:358:61//AQ005028  
 F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485  
 50 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//  
 AC003976  
 F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces  
 cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243  
 55 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey se-  
 quence.//2.8e-22:137:96//B80243  
 F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//  
 0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223  
 F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841  
 5 F-NT2RP4002078//RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030  
 F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062  
 F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437  
 10 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515  
 F-NT2RP4002791  
 F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383  
 15 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662  
 F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197  
 F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901  
 20 F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380  
 F-NT2RP5003492  
 F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365  
 25 F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703  
 F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236  
 30 F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178  
 F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631  
 35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934  
 F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510  
 F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933  
 F-OVARC1000013  
 40 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922  
 F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674  
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603  
 F-OVARC1000058  
 F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625  
 45 F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883  
 F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387  
 F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259  
 50 F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037  
 F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489  
 55 F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617  
 F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369  
 F-OVARC1000109  
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250  
 5 F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574  
 F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027  
 F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640  
 10 F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854  
 F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703  
 F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695  
 15 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764  
 F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557  
 F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604  
 20 F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332  
 F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910  
 25 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226  
 F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194  
 F-OVARC1000288 2.2e-22:181:83//J00345  
 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003  
 30 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574  
 F-OVARC1000309  
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236  
 35 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614  
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696  
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007  
 F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275  
 40 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693  
 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201  
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166  
 45 F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718  
 F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826  
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558  
 50 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165  
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284  
 F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678  
 55 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583  
 F-OVARC1000461  
 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

124:650:93//AF023451  
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221  
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191  
 5 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829  
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297  
 10 F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850  
 15 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024  
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510  
 F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic\_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820  
 20 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.4e-136:670:97//AL022069  
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985  
 25 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733  
 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942  
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414  
 30 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1 e-27:354:72//AC003973  
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775  
 35 F-OVARC1000605  
 F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648  
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772  
 40 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162  
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244  
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713  
 45 F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156  
 F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003  
 50 F-OVARC1000700  
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661  
 55 F-OVARC1000730  
 F-OVARC1000746  
 F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905



- F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403  
 F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552  
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
- 5 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691  
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469  
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
- 10 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584  
 F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963  
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125  
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086
- 15 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044  
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721  
 F-OVARC1000890  
 F-OVARC1000891
- 20 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494  
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
- 25 F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493  
 F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.2e-113:476:91//AC003983  
 F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848
- 30 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549  
 F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276  
 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850
- 35 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181  
 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270  
 F-OVARC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841
- 40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274  
 F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858  
 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785
- 45 F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910  
 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190  
 F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290
- 50 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021  
 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451  
 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149
- 55 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081  
 F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:6.1//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768  
 F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292  
 F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878  
 5 F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525  
 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657  
 F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529  
 10 F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153  
 F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333  
 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897  
 15 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782  
 F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178  
 20 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382  
 F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052  
 F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322  
 25 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004069  
 F-OVARC1001162  
 F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961  
 30 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141  
 F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823  
 F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315  
 F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323  
 35 F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001  
 F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195  
 F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486  
 40 F-OVARC1001200  
 F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334  
 F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235  
 F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078  
 45 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613  
 F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505  
 F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776  
 50 F-OVARC1001270  
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543  
 F-OVARC1001282//RPC111-60K8.TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857  
 55 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018  
 F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061

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F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986

F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504

5 F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071

F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402

F-OVARC1001342

10 F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456

F-OVARC1001357//Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297

F-OVARC1001360

15 F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811

F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801

F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819

20 F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287

F-OVARC1001399//CIT-HSP-229118.TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11 :104:87//AQ007611

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651

25 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426

F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudo-gene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714

F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387

30 F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687

F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482

35 F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277

F-OVARC1001480

F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140

40 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507

F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411

45 F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219

F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140

F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037

50 F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165

F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945

F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409

55 F-OVARC1001611

F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682

F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867  
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey se-  
 quence.//0.94:85:69//B92840  
 5 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING  
 DRAFT SEQUENCE.//1.9e-06:489:61//Z97651  
 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662  
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752  
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650  
 10 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522  
 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
 4.2e-149:706:98//U97670  
 15 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575  
 F-OVARC1001768  
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//  
 AC005066  
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:  
 76//AC004704  
 20 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey se-  
 quence.//0.98:214:61//AQ264481  
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last  
 coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene  
 downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-  
 25 151:712:99//AL023694  
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748  
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//  
 AC003662  
 30 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chro-  
 some X contains STS.//0.17:214:65//Z70224  
 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING  
 DRAFT SEQUENCE.//3.2e-55:379:82//AL031779  
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-  
 17:509:62//AC005609  
 35 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chro-  
 some X.//0.35:403:58//Z73361  
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey se-  
 quence.//2.4e-25:148:96//B94622  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611  
 40 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748  
 F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//  
 U51127  
 45 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-  
 29:350:74//AC005020  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 8.6e-56:300:96//AF061749  
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs,  
 complete sequence.//2.3e-10:253:66//AL031904  
 50 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069  
 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979  
 F-OVARC1001928  
 55 F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a.//  
 7.2e-12:83:98//Z60390  
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:  
 69//AF059179

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F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263  
 F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929  
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021  
 5 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995  
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934  
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15,  
 10 WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011  
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015  
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668  
 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483  
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.013:461:57//AC006241  
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427  
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey se-  
 20 quence.//2.3e-11:258:67//AQ055576  
 F-OVARC1002156  
 F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//1.8e-16:383:66//B11616  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568  
 25 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//AL017241  
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey se-  
 quence.//8.2e-10:158:75//AQ003859  
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585  
 30 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789  
 F-PLACE1000014  
 F-PLACE1000031//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821  
 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023  
 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177  
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508  
 40 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154  
 F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521  
 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6  
 45 unordered pieces.//5.2e-09:143:73//AC005848  
 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete se-  
 quence.//0.52:390:60//AC002389  
 F-PLACE1000094  
 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and  
 50 CpG Island, complete sequence.//4.4e-129:731:92//AL023580  
 F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291  
 F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-PLACE1000213  
 55 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504  
 F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

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F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813  
F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584  
5 F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp; tRNA-Val.//0.00013:369:59//X54011  
F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106  
F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350  
10 F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891  
F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163  
F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032  
15 F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074  
F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867  
F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899  
20 F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515  
F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189  
F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698  
25 F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382  
F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580  
F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491  
30 F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245  
F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276  
F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484  
35 F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409  
F-PLACE1000564  
F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//3.3e-46:631:68//M27877  
40 F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542  
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449  
F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276  
F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967  
45 F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201  
F-PLACE1000636  
F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265  
50 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896  
F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219  
F-PLACE1000712  
55 F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026  
F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109

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F-PLACE1000749//*Plasmodium falciparum* MAL3P7, complete sequence.//0.099:664:57//AL034559  
 F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589  
 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey se-  
 quence.//6.5e-08:93:89//B63806  
 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548  
 F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027  
 F-PLACE1000793//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read  
 cpg13d12.rt1c.//4.6e-09:71:100//Z64565  
 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:  
 10 72//AC002310  
 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 0.013:404:60//AC006158  
 F-PLACE1000849//H.sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read  
 cpg72a10.rt1a.//3.3e-09:82:92//Z62712  
 15 F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935  
 F-PLACE1000863//H.sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpg53d2.ft1b.//  
 7.3e-37:199:98//Z55621  
 F-PLACE1000909//H.sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read  
 cpg173f8.rt1a.//1.5e-17:128:92//Z57391  
 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate  
 receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181  
 F-PLACE1000948  
 F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//  
 1.0e-26:148:99//AQ194348  
 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572  
 F-PLACE1000979//H.sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpg76e8.rt1a.//  
 2.7e-10:84:94//Z55963  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267  
 F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011  
 30 F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey se-  
 quence.//0.99:277:58//B58681  
 F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357  
 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//  
 AC004741  
 35 F-PLACE1001024  
 F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey se-  
 quence.//1.1e-80:393:98//AQ108662  
 F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//  
 8.8e-40:483:66//AB013390  
 40 F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydroge-  
 nase.//1.2e-23:224:80//AJ224761  
 F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659  
 F-PLACE1001088  
 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485  
 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:  
 62//U81400  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:  
 71//AF022158  
 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702  
 F-PLACE1001168  
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603  
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the  
 gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene  
 55 for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6  
 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:  
 102:70//AL031177  
 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:

77//D14336  
 F-PLACE1001241  
 F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219  
 F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476  
 5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507  
 F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320  
 F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642  
 10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617  
 F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282  
 F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181  
 15 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342  
 F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614  
 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324  
 20 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319  
 F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340  
 F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177  
 25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087  
 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//8.2e-121:608:97//AC006241  
 30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384  
 F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106  
 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148  
 35 F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660  
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720  
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373  
 40 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786  
 F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667  
 45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_L\_16, complete sequence.//2.7e-139:482:96//AC005669  
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261  
 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817  
 50 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860  
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984  
 55 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959  
 F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037



- F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587
- 5 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341
- F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032
- F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//7.7e-159:788:97//AC005971
- 10 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165
- F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.1e-149:760:96//AC005921
- 15 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200
- F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
- 20 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051
- F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
- F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607
- F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221
- 25 F-PLACE1001745
- F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744
- F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243
- 30 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842
- F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972
- F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394
- 35 F-PLACE1001781 1.3e-08:238:65//AC005637
- F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474
- F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749
- 40 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953
- F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286
- 45 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177
- F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850
- F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244
- 50 F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408
- F-PLACE1001912
- F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935
- 55 F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361
- F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

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F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

15 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556

F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

30 F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

35 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324

40 F-PLACE1002319

F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956

F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623

F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//5.6e-05:474:59//AC005922

45 F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928

F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801

50 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262

F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

55 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060

F-PLACE1002499

- F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927  
 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
- 5 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256  
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774
- F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
- 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314  
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523
- F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443  
 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109
- 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537  
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785
- F-PLACE1002625  
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281
- 20 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180
- 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726  
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723
- F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273
- 30 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567  
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259
- F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
- 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
- F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295  
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
- 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//M27877  
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
- F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
- 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126  
 F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
- F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889
- 50 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120  
 F-PLACE1002962  
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558
- F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755
- 55 F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760  
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

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F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551  
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088  
 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829  
 5 F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200  
 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158  
 10 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875  
 F-PLACE1003108  
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219  
 F-PLACE1003145  
 15 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206  
 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495  
 F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934  
 20 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095  
 F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276  
 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466  
 25 F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954  
 F-PLACE1003249  
 F-PLACE1003256  
 F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317  
 30 F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429  
 F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877  
 F-PLACE1003334  
 35 F-PLACE1003342  
 F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715  
 40 F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095  
 F-PLACE1003366  
 F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558  
 F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247  
 45 F-PLACE1003375  
 F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878  
 F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680  
 50 F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588  
 F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388  
 F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470  
 55 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401  
 F-PLACE1003493  
 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

- F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859
- F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729
- 5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
- F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
- 10 F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
- F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
- F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
- 15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
- F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230
- 20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
- F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
- F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260
- 25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200
- F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356
- F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
- 30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
- F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
- F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478
- 35 F-PLACE1003669
- F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
- F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
- 40 F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920
- F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
- 45 F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297
- F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
- F-PLACE1003762
- F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
- 50 F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
- F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
- 55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
- F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

5 F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

10 F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

15 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108

F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

20 F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

25 F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

30 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

35 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

40 F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071

F-PLACE1004197

45 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

50 F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

55 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

F-PLACE1004274//H.sapiens CpG island DNA genomic Mse1 fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:

97//AF084830

F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U70855

F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpg55h1.ft1a.//12.4e-34:188:98//Z61632

F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

- 5 F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323  
F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577
- 10 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551  
F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959  
F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
- 15 F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766  
F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555  
F-PLACE1004751
- 20 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367  
F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713  
F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157
- 25 F-PLACE1004804  
F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710  
F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921
- 30 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613  
F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849  
F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313
- 35 F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825  
F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740  
F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819  
F-PLACE1004868
- 40 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344  
F-PLACE1004900  
F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184  
F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058
- 45 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571  
F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671  
F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989
- 50 F-PLACE1004937  
F-PLACE1004969  
F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843
- 55 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073  
F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833



F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:  
 590:61//AE001373  
 F-PLACE1005026  
 F-PLACE1005027  
 5 F-PLACE1005046  
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
 QUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//  
 10 AF059569  
 F-PLACE1005077  
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 complete sequence.//6.9e-29:253:77//AC004673  
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//  
 15 AC002316  
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-  
 146:734:96//AC005225  
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//  
 AC004476  
 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081  
 F-PLACE1005111  
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-  
 plete cds.//0.00051:287:63//L14320  
 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361  
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//  
 AC002451  
 F-PLACE1005176  
 F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey se-  
 30 quence.//0.99:211:63//AQ054651  
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey se-  
 quence.//2.7e-07:80:90//AQ074445  
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061  
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//  
 35 0.70:245:63//AC004965  
 F-PLACE1005243  
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812  
 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98//Z70695  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182  
 40 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183  
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//  
 M25757  
 F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole  
 Cg14.//1.0:128:67//AJ233621  
 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167  
 F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116  
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//  
 AC004794  
 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 5.5e-114:237:92//AC000380  
 F-PLACE1005373  
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//  
 AF017104  
 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991  
 F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6,  
 WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854  
 F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

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- F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581
- F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191
- 5 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878
- F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885
- 10 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394
- F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589
- F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485
- 15 F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038
- F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860
- F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925
- 20 F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354
- F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//9.3e-113:536:97//AC004707
- F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504
- 25 F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517
- F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126
- F-PLACE1005603
- 30 F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589
- F-PLACE1005623
- F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840
- 35 F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022
- F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255
- F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618
- 40 F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667
- F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457
- F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422
- 45 F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147
- F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635
- F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-25:290:75//AQ136844
- 50 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200
- F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517
- F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827
- 55 F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695
- F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-126:636:96//AF027156
- F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482

- F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150
- F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-105, complete sequence.//0.00080:663:58//AL010283
- 5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153
- F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432
- F-PLACE1005851
- 10 F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931
- F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226
- F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892
- 15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136
- F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026
- F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151
- 20 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405
- F-PLACE1005932
- F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpG165g2.ft1a.//8.3e-43:247:93//Z57153
- 25 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719
- F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236
- 30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081
- F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070
- F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925
- F-PLACE1005968
- 35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866
- F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090
- F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442
- 40 F-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521
- F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299
- 45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139
- F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906
- F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200
- 50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023
- F-PLACE1006129
- F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597
- F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015
- 55 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750
- F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

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F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200  
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239  
5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972  
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433  
F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658  
10 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125  
F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931  
F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803  
15 F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880  
F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327  
F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142  
20 F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400  
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548  
F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447  
25 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320  
F-PLACE1006318  
F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454  
30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721  
F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504  
F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559  
35 F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082  
F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232  
F-PLACE1006382  
F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085  
40 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029  
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735  
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129  
45 F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ 103347  
F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496  
F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118  
50 F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977  
F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744  
F-PLACE1006492  
F-PLACE1006506  
55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083  
F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

- F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510  
F-PLACE1006540  
F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998  
F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044
- 5 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670  
F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470
- 10 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589  
F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015  
F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276  
F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688
- 15 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790  
F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916
- 20 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048  
F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer/1.9e-135:378:99//AC005626
- 25 F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey sequence.//0.018:147:66//AQ039246  
F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426  
F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487
- 30 F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559  
F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513
- 35 F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272  
F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915  
F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033
- 40 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230  
F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350  
F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559  
F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
- 45 F-PLACE1006878  
F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120  
F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672
- 50 F-PLACE1006904  
F-PLACE1006917//H.sapiens CpG island DNA- genomic MseI fragment, clone 79g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175  
F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063
- 55 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308  
F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447  
F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//

U23921

F-PLACE1006961//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//*H.sapiens* ir1B mRNA.//7.1e-15:202:71//X63417

5 F-PLACE1006966//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

10 F-PLACE1007014//*Rattus norvegicus* equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat\*.//6.2e-131:775:89//Z82899

15 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.3e-131:652:97//AC005224

20 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//*Mus musculus* muskulin mRNA, complete cds.//4.1e-124:687:91//U72194

25 F-PLACE1007111//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

30 F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

35 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

40 F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082

F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

45 F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//AL011743

50 F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//*Dictyostelium discoideum* gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

55 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

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F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167  
F-PLACE1007386  
F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590  
5 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:  
93//AF093772  
F-PLACE1007416  
F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//  
AC003973  
10 F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433  
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391  
F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like pro-  
tease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117  
F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence,  
15 complete sequence.//2.5e-24:362:71//AC002302  
F-PLACE1007484  
F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//  
AF017370  
F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene  
20 similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311  
F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//3.6e-139:477:  
98//AC004231  
F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461  
F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxi-  
25 dase subunit 2 (cox2), and apocytochrome-b (cytb) genes, complete cds, and complete 9S rRNA gene and partial  
12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment,  
clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280  
F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:  
141:75//U31508  
30 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561  
F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240  
F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING  
DRAFT SEQUENCE.//3.6e-114:565:97//AL031665  
F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey se-  
35 quence.//2.0e-22:304:70//AQ111183  
F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.0:386:59//  
AC005245  
F-PLACE1007621  
F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library)  
40 complete sequence.//1.0e-88:276:96//AC006064  
F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132  
F-PLACE1007649  
F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
DRAFT SEQUENCE.//1.2e-21:567:64//AL023755  
45 F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120  
F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452  
F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483  
F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING  
DRAFT SEQUENCE.//0.0035:75:88//AL031662  
50 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243  
F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//  
1.0:510:58//AB005231  
F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro  
and pol pseudogenes.//4.8e-136:516:89//U86698  
55 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585  
F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-  
22:806:60//AC005484  
F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

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DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504  
 F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780  
 F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING  
 5 DRAFT SEQUENCE.//0.63:241:58//AL031749  
 F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:  
 87//AC005273  
 F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete se-  
 quence.//1.0e-113:739:86//AC003658  
 10 F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey se-  
 quence.//1.0e-47:254:97//AQ196438  
 F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//  
 AL006903  
 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,  
 15 WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010  
 F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309  
 F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey se-  
 quence.//0.015:279:61//AQ263271  
 20 F-PLACE1007877  
 F-PLACE1007897  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//  
 AB007956  
 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//  
 25 1.1e-59:310:81//AC003097  
 F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//  
 AC006157  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//  
 AF084530  
 30 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:  
 730:98//AF079529  
 F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//  
 U13262  
 F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758  
 35 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695  
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-  
 163:786:98//AC005628  
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:  
 84//L31840  
 40 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719  
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome  
 4p16.3.//4.0e-07:251:64//Z68883  
 F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey  
 sequence.//1.5e-30:166:99//B85883  
 45 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial  
 protein, partial cds.//7.5e-06:414:60//AF069163  
 F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867  
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosid-  
 ase Iix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586  
 50 F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
 DRAFT SEQUENCE.//3.6e-20:111:93//Z82199  
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-  
 88:866:73//D14849  
 F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING  
 55 DRAFT SEQUENCE.//0.0033:727:56//AL034397  
 F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450  
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-



162:791:97//AC005069  
 F-PLACE1008209  
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332  
 F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317  
 5 F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987  
 F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123  
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913  
 10 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779  
 F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432  
 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176  
 15 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579  
 F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352  
 20 F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512  
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.4e-11:403:64//AC005856  
 25 F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417  
 F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326  
 30 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688  
 F-PLACE1008424  
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864  
 35 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317  
 F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479  
 F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589  
 40 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526  
 F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014  
 45 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494  
 F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778  
 F-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555  
 50 F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097  
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997  
 55 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571  
 F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

- F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077
- F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373
- 5 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967
- F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836
- F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732
- 10 F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356
- F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23 :299:64//D38595
- F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333
- 15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732
- F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406
- F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199
- 20 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260
- F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25 :244:71//AC003037
- 25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543
- F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549
- F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643
- 30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933
- F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668
- F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920
- 35 F-PLACE1008854
- F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209
- F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539
- 40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660
- F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308
- F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042
- 45 F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312
- F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309
- F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences.//5.9e-15:710:60//M34651
- F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727
- 50 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117
- F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137
- 55 F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861
- F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1.//4.7e-70:463:80//D00766

F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241

F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073

5 F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919

F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence.//0.027:630:58//AC006016

F-PLACE1009094

F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85:726:76//M36515

10 F-PLACE1009110

F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752

F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586

15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:59//D25215

F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929

F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031

20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair.//1.0:173:60//X52222

F-PLACE1009166

F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070

F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library)

25 complete sequence.//2.9e-19:288:72//AC004805

F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.//0.053:388:60//AB008266

F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242

F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881

30 F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198

F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203

F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945

35 F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024

F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192

40 F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399

F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015

F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811

45 F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311

F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:74//M27878

50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494

F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.6e-150:701:99//AC005919

F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:88//AF046700

F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//0.012:582:56//AL022022

55 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872

F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.9e-31:264:81//AF046660

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F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I30536  
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//1.9e-142:704:97//AC004531  
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:235:68//AC004601  
 5 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.9e-83:171:92//U91321  
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160  
 10 F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//AF041862  
 F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587  
 15 F-PLACE1009571//RPC111-60K12.TK RPC111 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869  
 F-PLACE1009581  
 F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959  
 20 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049  
 F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824  
 25 F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157  
 F-PLACE1009621  
 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248  
 30 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308  
 F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816  
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159  
 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177  
 35 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534  
 F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011  
 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109  
 F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026  
 40 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024  
 F-PLACE1009794  
 F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996  
 45 F-PLACE1009845  
 F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620  
 F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397  
 50 F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427  
 F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431  
 55 F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369  
 F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005  
 F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-

- QUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529  
 F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066  
 F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655  
 5 F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026  
 F-PLACE1009971  
 F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311  
 10 F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029  
 F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288  
 F-PLACE1010023  
 15 F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775  
 F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692  
 20 F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114  
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482  
 F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540  
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925  
 25 F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence.//4.8e-07:124:78//AQ101268  
 F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411  
 F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506  
 30 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569  
 F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928  
 F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164  
 F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636  
 35 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757  
 F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//2.4e-15:197:72//AC004973  
 F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967  
 40 F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829  
 F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377  
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917  
 F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710  
 45 F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029  
 F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464  
 F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005  
 50 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468  
 F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837  
 F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178  
 55 F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252  
 F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

- F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985
- F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675
- 5 F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825
- F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927
- F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081
- F-PLACE1010492
- 10 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695
- F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145 :684:98//AR016417
- F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677
- F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831
- 15 F-PLACE1010579//Homo sapiens full-length insert cDNA Y123D12.//3.9e-19:147:89//AF075014
- F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125
- F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186
- 20 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308
- F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558
- F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107
- 25 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846
- F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682
- F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872
- 30 F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069
- F-PLACE1010661
- F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960
- 35 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376
- F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583
- 40 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678
- F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864
- F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609
- 45 F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921
- F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061
- F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221
- F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252
- 50 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384
- F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380
- F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283
- 55 F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229
- F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868

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F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182  
 F-PLACE1010891  
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997  
 F-PLACE1010900  
 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687  
 F-PLACE1010917  
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126  
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243  
 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247  
 F-PLACE1010947  
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965  
 F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//0.00074:421:60//AL010226  
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696  
 F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.00037:257:64//AL008972  
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348  
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669  
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636  
 F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686  
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049  
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548  
 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687  
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684  
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249  
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60//B19698  
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305  
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:87//AC004893  
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443  
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-43:447:72//AC002288  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965  
 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014  
 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

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F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770

F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647

5 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.r1b.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

10 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310

15 F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

20 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

25 F-PLACE1011503

F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

30 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477

35 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729

40 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374

45 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

50 F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

55 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003

F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944



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F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147

5 F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

10 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

15 F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

F-PLACE1011995//Homo sapiens Xq28 BAC RPCI1-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054

20 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256

F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837

F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

25 F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

30 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

40 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

50 F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

55 F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

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F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166

5 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070

F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995

F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701

F-PLACE2000170

10 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005

F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//0.98:201:64//AC004032

F-PLACE2000187

15 F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58/B75888

F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003

20 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577

F-PLACE2000274//Anthracis crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308

25 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//US2064

F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021

F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747

30 F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554

35 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829

F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006

F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849

40 F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973

F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182

45 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776

F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909

50 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:63//X06967

F-PLACE2000399

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238

55 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984

F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792

F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949  
 F-PLACE2000427  
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:  
 67//AC005821  
 5 F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999  
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492  
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:  
 80//AC006025  
 10 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-  
 05:330:63//AC002300  
 F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-  
 168:816:97//AC005740  
 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete se-  
 15 quence.//4.3e-33:296:79//AC002037  
 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//  
 3.4e-59:598:74//AC005057  
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602  
 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187  
 20 F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075  
 F-PLACE3000029  
 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267  
 F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-  
 17:250:74//AC005368  
 25 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006  
 F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670  
 F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668  
 F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//  
 30 AC005695  
 F-PLACE3000136  
 F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//0.011:294:62//AL033520  
 F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662  
 35 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the  
 DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053  
 F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474  
 F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:  
 98//AC005277  
 40 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
 R32804, complete sequence.//2.2e-81:783:74//AC003682  
 F-PLACE3000157  
 F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500  
 F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey se-  
 45 quence.//0.080:259:59//B50878  
 F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//  
 AC006130  
 F-PLACE3000194  
 F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//  
 50 AL003352  
 F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING  
 DRAFT SEQUENCE.//0.0019:277:58//Z82207  
 F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//  
 AC005013  
 55 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII inter-  
 genic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982  
 F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//  
 AC004086

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F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.2e-135:721:91//AC005231

5 F-PLACE3000226

F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

10 F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548

15 F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328

20 F-PLACE3000310

F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379

F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:68//AC005822

25 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642

F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055

30 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732

35 F-PLACE3000353

F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

40 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

45 F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023

50 F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

55 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

0.0018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284

F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence.//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843

F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08 :692:60//I39845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131

F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926

F-PLACE4000052//M.musculus abcl mRNA.//1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311

F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158

F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430

F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673

F-PLACE4000252

F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200

F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259

F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075

F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296

F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401

F-PLACE4000367

F-PLACE4000369  
 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661  
 F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649  
 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540  
 F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984  
 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200  
 F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346  
 F-PLACE4000450  
 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065  
 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//4.1e-34:351:70//AC005821  
 F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537  
 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865  
 F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929  
 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645  
 F-PLACE4000548  
 F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747  
 F-PLACE4000581  
 F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474  
 F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418  
 F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281  
 F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039  
 F-PLACE4000650  
 F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267  
 F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816  
 F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577  
 F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312  
 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554  
 F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616  
 F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797  
 F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561  
 F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637  
 F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353  
 F-THYRO1000035//Human Chromosome X clone bWDX187, complete sequence.//1.2e-39:303:83//AC004383  
 F-THYRO1000040  
 F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383  
 F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557  
 F-THYRO1000085  
 F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606  
 F-THYRO1000107

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- F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403
- F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055
- 5 F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724
- F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142
- F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096
- 10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574
- F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331
- F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419
- 15 F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207
- F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
- F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746
- 20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
- F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
- F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
- F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
- 25 F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
- F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
- F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055
- 30 F-THYRO1000270
- F-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
- F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
- F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
- 35 F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
- F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333
- F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091
- 40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080
- F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668
- F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019
- F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672
- 45 F-THYRO1000395//Drosophila melanogaster ring canal protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483
- F-THYRO1000401 3.2e-116:504:80//AF051908
- F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308
- 50 F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573
- F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229
- 55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196
- F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740
- F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

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F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

F-THYRO 1000505

5 F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYRO1000570

10 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

15 F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

20 F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-68:468:84//AC005696

F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

25 F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

30 F-THYRO1000699//RPC111-50D4.TK RPC111 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

35 F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

40 F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

45 F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

50 F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

55 F-THYRO1000843

F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:



64//AF008573  
 F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477  
 F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING  
 5 DRAFT SEQUENCE.//2.8e-18:186:80//AL031720  
 F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529  
 10 F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836  
 F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229  
 F-THYRO1000952  
 F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846  
 15 F-THYRO1000975//Plasmodium falciparum Topoll gene.//0.32:491:58//X79345  
 F-THYRO1000983//Mvfw9A3 exon amplification products from BACs in Mvfw region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457  
 F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313  
 20 F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588  
 F-THYRO1001003  
 F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//1.1e-55:543:72//AC003695  
 25 F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799  
 F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320  
 30 F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787  
 F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522  
 35 F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595  
 F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996  
 F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486  
 40 F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178  
 F-THYRO1001173  
 F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953  
 45 F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330  
 F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925  
 F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300  
 50 F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036  
 F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496  
 F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086  
 F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237  
 55 F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693  
 F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

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F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114  
 F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025  
 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288  
 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905  
 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//7.6e-168:821:97//AC005660  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607  
 10 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239  
 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845  
 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852  
 15 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:82//AF064635  
 F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126  
 F-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553  
 20 F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384  
 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265  
 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001  
 25 F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449  
 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666  
 F-THYRO1001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687  
 30 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074  
 F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056  
 F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105  
 35 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572  
 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498  
 F-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808  
 40 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//2.9e-26:393:68//AC005863  
 F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576  
 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381  
 45 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950  
 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827  
 F-THYRO1001661  
 50 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089  
 F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071  
 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857  
 F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745  
 55 F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500  
 F-THYRO1001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYRO1001745  
 F-THYRO1001746  
 F-THYRO1001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021  
 5 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626  
 F-THYRO 1001809  
 F-THYRO1001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING  
 DRAFT SEQUENCE.//1.3e-175:841:98//AL033526  
 F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//  
 10 AC003664  
 F-THYRO1001895  
 4.4e-13:248:68//AB012576  
 F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//  
 AC005058  
 15 F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749  
 F-Y79AA1000013  
 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//  
 AC006027  
 20 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521  
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on  
 chromosome X contains EST.//5.3e-10:117:83//Z72005  
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893  
 25 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 complete sequence.//1.4e-165:732:99//AL031864  
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-  
 20:339:65//AC005115  
 30 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
 3.7e-72:397:93//AC004854  
 F-Y79AA1000230  
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232  
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACp-1) gene, complete cds.//  
 35 0.0099:547:58//U78522  
 F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207  
 F-Y79AA1000313  
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey se-  
 quence.//5.9e-07:173:69//B55085  
 40 F-Y79AA1000342//RPC111-57J6.TK.1 RPC111 Homo sapiens genomic clone R-57J6, genomic survey sequence.//  
 5.2e-27:151:99//AQ115511  
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987  
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692  
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-  
 45 21:129:85//AC005484  
 F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//  
 0.00016:53:98//Z56610  
 F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING  
 DRAFT SEQUENCE.//0.069:366:59//AL031747  
 50 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061  
 F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a.//  
 2.0e-36:194:98//Z63378  
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete  
 cds.//8.5e-121:696:89//U41736  
 55 F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693  
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//  
 0.67:111:72//AC004980

F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503  
F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193

5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972  
F-Y79AA1000574//M.musculus tex23 mRNA (5'region).//1.8e-23:291:75//X80424  
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080  
F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503  
F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942

10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080  
F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172  
F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023  
F-Y79AA1000774

15 F-Y79AA1000782  
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799  
F-Y79AA1000794//H.sapiens CpG island DNA genomic MseI fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120  
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085

20 F-Y79AA1000802  
F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642  
F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538  
F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING

25 DRAFT SEQUENCE.//1.5e-08:249:69//AL022315  
F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757  
F-Y79AA1000850  
F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203

30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314  
F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253  
F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397

35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165  
F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823  
F-Y79AA1001023  
F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329

40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682  
F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701  
F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314

45 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452  
F-Y79AA1001078  
F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173  
F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015

50 F-Y79AA1001167  
F-Y79AA1001177//M.musculus mRNA for NfiX1-protein.//4.0e-10:398:64//Y07688  
F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING

55 DRAFT SEQUENCE.//1.1e-113:666:90//Z93015  
F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492  
F-Y79AA1001216  
F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//

- AL021841  
F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263
- 5 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892  
F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497  
F-Y79AA1001299//Human Ini1 mRNA, complete cds.//6.7e-115:323:93//U04847
- 10 F-Y79AA1001312  
F-Y79AA1001323  
F-Y79AA1001384  
F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322  
F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583
- 15 F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924  
F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497  
F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430
- 20 F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336  
F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183  
F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151
- 25 F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267  
F-Y79AA1001581//FMR1 (CGG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494  
F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434
- 30 F-Y79AA1001594  
F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861  
F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583
- 35 F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860  
F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468  
F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743
- 40 F-Y79AA1001692//Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712  
F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polypeptide (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136  
F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943
- 45 F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240  
F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017  
F-Y79AA1001805//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.r1c.//2.6e-13:88:100//Z64565
- 50 F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297  
F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369  
F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388
- 55 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164  
F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

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F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654  
F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186  
5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184  
F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340  
10 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214  
F-Y79AA1002089  
F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548  
15 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014  
F-Y79AA1002115  
F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693  
F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358  
20 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260  
F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397  
F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719  
25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615  
F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043  
F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738  
30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045  
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592  
F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015  
35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555  
F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886  
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534  
F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877  
F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101  
40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208  
F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920  
F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662  
45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385  
F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196  
F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917  
50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116  
F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022  
F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

55 Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

[0304] Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

5

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

10

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953  
 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//  
 Z88864

R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapiens genomic clone R-77G23, genomic survey se-  
 quence.//1.3e-56:292:97//AQ268240

15

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-  
 41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete  
 sequence.//4.7e-30:229:84//AC003684

20

R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//  
 AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-  
 37:289:83//AC005060

25

R-nnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//  
 L43631

R-HEMBA1000158

R-nnnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904

30

R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

35

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:  
 79//AF001548

R-nnnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate  
 receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181

40

R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:  
 319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ri-  
 bosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

45

R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15,  
 WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012

R-nnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete  
 sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270

50

R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:  
 267:82//AC003046

R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//  
 AC004223

55

R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey se-  
 quence.//1.0:215:61//B95105

R-nnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131

R-nnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:  
 546:90//U16802

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R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496  
R-nnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505  
5 R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
DRAFT SEQUENCE.//2.0e-33:399:72//AL031667  
R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing  
Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147  
R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829  
R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086  
10 R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//  
AC006012  
R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene sim-  
ilar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS  
and a CpG island, complete sequence.//1.9e-69:355:97//AL031587  
15 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-  
66:410:89//AC006116  
R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 un-  
ordered pieces.//2.0e-43:363:81//AC002993  
R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//  
20 AC005053  
R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//  
AC004582  
R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains  
inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575  
25 R-HEMBA1000411  
R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465  
R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey se-  
quence.//4.4e-12:98:92//AQ078233  
R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
30 complete sequence.//2.0e-93 :526:90//Z95400  
R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
2.7e-07:452:60//AC004826  
R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733  
R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, com-  
35 plete sequence.//2.6e-05:174:70//AL010226  
R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-bind-  
ing protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane  
protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, com-  
plete cds; and unknown genes.//0.013:212:63//AF049236  
40 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//  
AC004839  
R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220  
R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//  
AC005104  
45 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500  
R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278  
R-HEMBA1000491  
R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, com-  
plete sequence.//1.7e-08:440:60//AL009014  
50 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858  
R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chro-  
mosome X.//1.1e-25:248:80//Z70280  
R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey se-  
55 quence.//0.0035:293:61//B49544  
R-HEMBA1000519  
R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//  
0.30:255:63//AC006232



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R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

5 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

10 R-HEMBA1000557//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

15 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

20 R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

25 R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

30 R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.rt1a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

45 R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850

50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

55 R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

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R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.

5 Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

10 R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

15 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

20 R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

25 R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

30 R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

35 R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

40 R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

45 R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

50 R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

55 R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

10 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

15 R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

20 R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

25 R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004

R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046

30 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318

R-HEMBA1001080

R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586

35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105

R-HEMBA1001099

R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527

40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833

R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551

R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511

R-HEMBA1001133

R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241

45 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077

R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304

R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398

50 R-HEMBA1001197

R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

55 R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666

R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

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R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905

R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491

5 R-HEMBA1001265//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042

R-HEMBA1001286

R-HEMBA1001289

10 R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882

R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222

R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258

15 R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744

R-HEMBA1001310

R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504

20 R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240

R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368

25 R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509

R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216

30 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238

R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241

R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542

35 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865

R-HEMBA1001383

R-HEMBA1001387

R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073

40 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960

R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050

R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35 :464:68//AL034380

45 R-HEMBA1001407

R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981

R-HEMBA1001413

R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732

50 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146

R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054

55 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527

R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

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R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385  
R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065  
5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855  
R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//2.7e-08:316:62//AC005324  
R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//0.57:219:60//  
10 AC005208  
R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840  
R-HEMBA1001478  
R-HEMBA1001497  
15 R-HEMBA1001510/Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337  
R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753  
R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//  
20 AC004549  
R-HEMBA1001522  
R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258  
R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine  
25 deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053  
R-HEMBA1001557  
R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383  
R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040  
R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//  
30 AC004453  
R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506  
R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276  
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012  
35 R-HEMBA1001589  
R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483  
R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177  
40 R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693  
R-nnnnnnnnnnnn/HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688  
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270  
45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484  
R-nnnnnnnnnnnn  
R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368  
50 R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808  
R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740  
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247  
55 R-HEMBA1001675  
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

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R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593

R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801

5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598

R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886

R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577

10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250

R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781

R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261

15 R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799

R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959

20 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067

R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084

25 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153

R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//3.8e-39:331:80//AC006121

R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554

30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740

R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575

35 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222

R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506

R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977

40 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969

R-HEMBA1001809

R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025

45 R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612

R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107

R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118

50 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107

R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507

R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871

R-HEMBA1001847

55 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517

R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

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R-nnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

5 R-HEMBA1001896

R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

R-HEMBA1001913

10 R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

15 R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

20 R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

25 R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

30 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence.//4.9e-06:153:71//AQ240461

35 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

40 R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

45 R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203

R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

50 R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

R-HEMBA1002084//CIT-HSP-2357LI1.TR CIT-HSP Homo sapiens genomic clone 2357LI1, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

55 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

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non-small cell lung cancer , segment 11/11.//1.1e-70:559:79//AB020868  
 R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602  
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//  
 5 AC005954  
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//  
 AC004848  
 R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276  
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-  
 10 23:183:80//AC006026  
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimu-  
 lation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP  
 A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819  
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378  
 15 R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068  
 R-nnnnnnnnnnnnn  
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:  
 80//AC004841  
 R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573  
 20 R-HEMBA1002495//CITBI-E1-2515J10. TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey se-  
 quence.//1.0:122:68//AQ261762  
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 2.8e-22:210:78//AC004963  
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//  
 25 AC003043  
 R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972  
 R-HEMBA1002515  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923  
 30 R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792  
 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658  
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378  
 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957  
 35 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409  
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS,  
 GSS, complete sequence.//7.1e-44:192:80//AL008634  
 R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587  
 R-HEMBA1002583  
 40 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains  
 the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein  
 CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete se-  
 quence.//9.4e-42:248:88//Z95152  
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//  
 45 AC004510  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351  
 R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275  
 R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247  
 50 R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567  
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//  
 AC004839  
 R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs  
 and GSSs, complete sequence.//1.2e-61:280:92//AL022323  
 55 R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING  
 DRAFT SEQUENCE.//3.2e-41:325:81//AL031772  
 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008  
 R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORK-

ING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421  
 R-nnnnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281  
 R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:146:70//AC004503  
 5 R-HEMBA1002696  
 R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982  
 R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873  
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521  
 10 R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109  
 R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525  
 R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694  
 15 R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883  
 R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810  
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126  
 20 R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140  
 R-HEMBA1002777  
 R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139  
 R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344  
 25 R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560  
 R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261  
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185  
 30 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043  
 R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041  
 R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:97//AC004707  
 35 R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506  
 R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:85//AC005562  
 40 R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557  
 R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836  
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261  
 45 R-HEMBA1002921  
 R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//4.6e-19:139:78//AB020875  
 R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681  
 50 R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584  
 R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532  
 55 R-HEMBA1002939  
 R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952  
 R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020

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R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005  
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.2e-38:300:83//AC005553  
5 R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012  
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579  
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128  
10 R-nnnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXd691, complete sequence.//0.00040:504:59//AC004386  
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614  
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406  
15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194  
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026  
R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839  
20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694  
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983  
25 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182  
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962  
R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302  
30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136  
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975  
35 R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054  
R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673  
40 R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798  
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039  
R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213  
45 R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598  
R-HEMBA1003117  
R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329  
50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472  
R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861  
55 R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024  
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670  
R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

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R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459  
R-HEMBA1003197  
R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162  
5 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
5.4e-44:291:83//AC005480  
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//  
AC000118  
10 R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:  
118:69//AC006148  
R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0:00014:59:91//AQ128202  
R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y43F8,  
WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393  
15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey  
sequence.//0.42:167:64//B83610  
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey se-  
quence.//3.6e-36:195:81//AQ037231  
20 R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356  
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709  
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete se-  
quence.//1.0e-32:255:84//AC002549  
25 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308  
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library)  
complete sequence.//1.1e-34:286:74//AC002395  
R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
ordered pieces.//1.8e-53:428:83//AC005840  
30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109  
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey se-  
quence.//2.9e-20:337:65//AQ003073  
R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662  
35 R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete se-  
quence.//0.00019:334:60//AB017061  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//  
AB001872  
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,  
GSS, complete sequence.//0.60:274:61//AL022153  
40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//  
AC005099  
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//  
2.2e-44:268:90//AC005081  
45 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//  
AF026029  
R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567  
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600  
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//  
AC002558  
50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alter-  
natively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a  
PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta,  
PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs,  
STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721  
55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:  
309:88//AC004651  
R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

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R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212

R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993

5 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549

R-nnnnnnnnnnnnn

R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321

10 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879

R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696

R-HEMBA1003461

15 R-HEMBA1003463

R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041

R-HEMBA1003528

R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454

20 R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701

R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453

R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153

25 R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718

R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913

R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416

30 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036

R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450

R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914

35 R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ209302

R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123

R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774

40 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715

R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480

45 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153

R-HEMBA1003615

R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139

50 R-HEMBA100362111\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599

R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980

55 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219

R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454

R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693  
 R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559  
 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382  
 R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.6e-117:588:96//AC005746  
 R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222  
 R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065  
 R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313  
 R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872  
 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466  
 R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707  
 R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406  
 R-HEMBA1003714  
 R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136  
 R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353  
 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699  
 R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158  
 R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634  
 R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179  
 R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876  
 R-HEMBA1003760  
 R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343  
 R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259  
 R-HEMBA1003784  
 R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1 e-49:390:72//AC004455  
 R-HEMBA1003803  
 R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596  
 R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781  
 R-HEMBA1003807//Bovine dinucleotide microsatellite HUII17.//5.4e-18:194:78//M96348  
 R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115  
 R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624  
 R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929  
 R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

5 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

10 R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368

15 R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718

R-HEMBA1003939

R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904

R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619

20 R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560

R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668

R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132

25 R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414

R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060

R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

30 R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

R-HEMBA1004000

35 R-HEMBA1004011

R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575

40 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016

45 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

50 R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

55 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

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R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

5 R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

10 R-HEMBA1004150//CITBI-E1-251712.TR CITBI-E1 Homo sapiens genomic clone 251712, genomic survey sequence.//0.56:379:59//AQ277616

R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855

15 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569

R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552

R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304

20 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488

R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748

R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275

25 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927

R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763

R-HEMBA1004241

30 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011

R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903

R-HEMBA1004264

35 R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854

R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831

R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081

40 R-HEMBA1004276

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795

R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence.//2.3e-37:248:76//AQ266668

45 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174

R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206

R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088

50 R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611

R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933

R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600

55 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987

R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds.//3.3e-14:238:69//AF082024

R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.8e-



21:291:71//AC004638  
 R-HEMBA1004341  
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667  
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, ge-  
 5 nomic sequence, complete sequence.//7.0e-38:287:82//AC003002  
 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611  
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949  
 R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey se-  
 quence.//0.010:334:61//B55811  
 10 R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540  
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124  
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:  
 69//AC004057  
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//  
 15 AC005030  
 R-HEMBA1004408  
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200  
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete  
 sequence bases 1..333303.//7.2e-32:460:68//AJ011930  
 20 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 3.9e-113:581:96//AC004846  
 R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876  
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//  
 25 AC006012  
 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:  
 513:59//AE001370  
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK:372\_K\_20, complete sequence.//2.0e-08:245 :  
 66//AC005951  
 30 R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING  
 DRAFT SEQUENCE.//4.2e-81:582:83//Z84487  
 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266  
 R-HEMBA1004509  
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230  
 35 R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330  
 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey se-  
 quence.//1.7e-16:116:93//B73329  
 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457  
 40 R-HEMBA1004573  
 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome  
 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:  
 60//Z68279  
 R-HEMBA1004586  
 45 R-HEMBA1004586//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551  
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//  
 AB007970  
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library)  
 50 complete sequence.//4.4e-13:527:63//AC004805  
 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866  
 R-HEMBA1004632  
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 7.7e-117:573:98//AC005534  
 55 R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076  
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//  
 0.00013:501:58//AC005171  
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432  
 R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING  
 DRAFT SEQUENCE.//4.4e-12:110:88//Z93241  
 5 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//  
 Z99291  
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//  
 0.86:309:57//AB006702  
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//  
 0.29:331:61//B97342  
 10 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559  
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-  
 49:497:76//AC004638  
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.6e-38:362:  
 79//AC005562  
 15 R-HEMBA1004725  
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:  
 79//AC002085  
 R-HEMBA1004733  
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene  
 20 for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island,  
 ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395  
 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017  
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:  
 81//AC004953  
 25 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950  
 R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING  
 DRAFT SEQUENCE.//3.3e-39:281:85//AL031121  
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//  
 30 L06498  
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains his-  
 tone genes H2A/1,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG  
 island.//1.8e-08:516:59//AL021807  
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:  
 35 72//AC004057  
 R-HEMBA1004763  
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-  
 notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
 40 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310  
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:  
 476:61//AE001371  
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete  
 sequence.//5.0e-08:113:80//AC003047  
 45 R-HEMBA1004776  
 R-HEMBA1004778//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567  
 R-nnnnnnnnnnnn/HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic  
 clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855  
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728  
 50 R-HEMBA1004806  
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-  
 20:333:69//AC005015  
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 55 Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002  
 R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//7.6e-80:297:85//  
 X53744

- R-HEMBA1004850  
 R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201  
 R-HEMBA1004864
- 5 R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297  
 R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826
- 10 R-HEMBA1004889//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943  
 R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:7711AC005972  
 R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052
- 15 R-HEMBA1004918//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554  
 R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994  
 R-HEMBA1004929
- 20 R-HEMBA1004930//Homo sapient chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848  
 R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755  
 R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic-clone 2021I16, genomic survey sequence.//0.66:268:62//B65345
- 25 R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849  
 R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341  
 R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408
- 30 R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249  
 R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982  
 R-HEMBA1004973//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656
- 35 R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495  
 R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509  
 R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614
- 40 R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389  
 R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224  
 R-HEMBA10050087//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663
- 50 R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474  
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548  
 R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),
- 55

- H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179  
 R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:94//AC004596
- 5 R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650  
 R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819  
 R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404
- 10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//AC004675  
 R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030  
 R-HEMBA1005075
- 15 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156  
 R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423  
 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561
- 20 R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340  
 R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336
- 25 R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345  
 R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834  
 R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407
- 30 R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279  
 R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594
- 35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276  
 R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205  
 R-HEMBA1005219  
 R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854
- 40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617  
 R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154  
 R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947
- 45 R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548  
 R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.6e-105:437:97//AC005837
- 50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630  
 R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914  
 R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887
- 55 R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120  
 R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//

1.5e-58:445:78//AC006146  
 R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337  
 R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389  
 5 R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030  
 R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181  
 R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.9e-112:577:95//AC005803  
 10 R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722  
 R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412  
 R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915  
 15 R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997  
 R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142  
 R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542  
 20 R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670  
 R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379  
 25 R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958.  
 R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722  
 30 R-HEMBA1005411//RPC111-66N19.TK RPC111 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442  
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248  
 R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196  
 35 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391  
 R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054  
 R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894  
 40 R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212  
 R-HEMBA1005472//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524  
 45 R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377  
 R-HEMBA1005497  
 R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957  
 50 R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826  
 R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509  
 R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811  
 55 R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320  
 R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384  
 R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.8e-84:309:99//AB020860

5 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431

10 R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989

15 R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631//AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538

20 R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171

R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499

R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

25 R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//2.2e-28:262:79//AC005746

30 R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446

R-HEMBA1005606//Human PAC clone DJ0093103 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

35 R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

40 R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13O15, genomic survey sequence.//1.0e-28:153:82//B73293

45 R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450

50 R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406

55 R-HEMBA1005705//RPCI11-13O14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13O14, genomic survey sequence.//0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.

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Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

5 R-nnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

10 R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

15 R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

20 R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPC13-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

25 R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

30 R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

35 R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//5.4e-79:403:97//AQ147357

40 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

45 R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

50 R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

55 R-nnnnnnnnnnnn

R-HEMBA1006081

R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

R-HEMBA1006091  
R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains syn-  
apsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//  
1.6e-36:354:77//AL009172

5 R-HEMBA1006108  
R-HEMBA1006121  
R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs  
and polymorphic CA repeat.//1.3e-12:327:64//Z95113  
R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

10 R-HEMBA1006130//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//  
AC005777  
R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500  
R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

15 R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:  
574:98//AF048693  
R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//  
U28217  
R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//  
AC004491

20 R-HEMBA1006198//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567  
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557  
R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567  
R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:  
25 71//U91323  
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384  
R-HEMBA1006259//RPC111-44N14.TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey se-  
quence.//1.5e-48:348:85//AQ203161  
R-HEMBA1006268

30 R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two  
Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//  
2.8e-73:273:87//AL023753  
R-HEMBA1006283//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770  
R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240

35 R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//0.97:447:59//  
AC004585  
R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161  
R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415  
R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2  
40 ordered pieces.//8.6e-37:288:84//AC005412  
R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-  
29:132:81//AF076183  
R-HEMBA1006328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING  
DRAFT SEQUENCE.//3.3e-50:340:75//AL034429

45 R-HEMBA1006334  
R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945  
R-HEMBA1006347//Human prostaticin gene, complete cds.//1.8e-78:170:100//U33446  
R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682  
R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey  
50 sequence.//4.7e-74:576:82//AQ277951  
R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080  
R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//  
AC005239  
R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989  
55 R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//1.5e-47:  
336:86//AC005914  
R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-  
67:501:83//AC005609



- R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence.//4.4e-37:319:76//AC002119
- R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253
- 5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//4.1e-116:572:97//AF107885
- R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:578:97//AL031781
- 10 R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017
- R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162
- 15 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075
- R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398
- 20 R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364
- R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//11.1e-14:354:63//AC002052
- R-HEMBA1006471
- 25 R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502
- R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742
- R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701
- 30 R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089
- R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989
- R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//4.3e-112:572:95//AC005828
- 35 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994
- R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015
- 40 R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929
- R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566
- R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304
- 45 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526
- R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525
- R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007
- 50 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603
- R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.4e-64:551:78//U06944
- R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554
- 55 R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421
- R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357
- R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032

R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875

R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709

5 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031

R-HEMBA1006612

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737

10 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudo-genes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284

R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 202O8, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848

15 R-HEMBA1006635//\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572

R-HEMBA1006639

R-HEMBA1006643

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282

20 R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089

R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390

R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625

25 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776

R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551

R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608

30 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096

R-HEMBA1006696

R-HEMBA1006708

R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674

35 R-HEMBA1006717

R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828

R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108

40 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951

R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752

45 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551

R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.3e-46:305:87//AC005701

R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323

50 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317

R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.1e-43:355:801//AC006120

R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483

55 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854

R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//3.0e-08:84:90//AC004797

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R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023

R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//0.70:206:65//AC005668

5 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217

R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074

R-HEMBA1006885//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026

R-HEMBA1006885 4.2e-14:379:63//AG006839

10 R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395

R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154

R-HEMBA1006926

15 R-HEMBA1006929//HS\_3244\_A2\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500

R-HEMBA1006936

R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853

20 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841

R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518

R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302

25 R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701

R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271

30 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406

R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558

R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.6e-41:437:71//AC005277

35 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088

R-HEMBA1007045

R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006

R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056

40 R-HEMBA1007062

R-HEMBA1007066

R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//2.0e-66:476:85//AC006141

R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//1.0e-38:179:82//AC005325

45 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015

R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385

R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803

50 R-HEMBA1007113//Homo sapiens (subclone 6\_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392

R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

R-HEMBA1007147//H.sapiens CpG island DNA genomic MseI fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246

55 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239

R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//

AC004875  
 R-nnnnnnnnnnnr/Homo sapiens epsin 2a mRNA, complete cds.//5.1e-103:529:94//AF062085  
 R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE,  
 129 ordered pieces.//5.4e-106:537:96//AC005911  
 5 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//4.1e-39:262:80//AC003035  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61:332:95//D86987  
 R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains  
 ESTs STS and CpG island.//1.9e-50:436:81//Z93023  
 10 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96:471:97//AB018340  
 R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//0.011:  
 349:62//AC004777  
 R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence.//2.8e-10:224:70//  
 AC004856  
 15 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence.//3.4e-53:362:86//AC005924  
 R-HEMBA1007273  
 R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//  
 AJ235273  
 20 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.99:288:60//  
 AJ235272  
 R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS,  
 CpG island, complete sequence.//7.4e-107:554:95//AL031003  
 R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U39994  
 25 R-HEMBA1007301  
 R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08:524:58//Y14425  
 R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SE-  
 QUENCE.//3.4e-16:244:71//AP000043  
 R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383:85//  
 30 AC005251  
 R-HEMBA1007327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING  
 DRAFT SEQUENCE.//1.6e-38:533:71//Z96804  
 R-HEMBA1007341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING  
 DRAFT SEQUENCE.//3.6e-21:394:66//AL023513  
 35 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence.//1.7e-15:190:73//AC003080  
 R-HEMBA1007347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING  
 DRAFT SEQUENCE.//2.2e-47:455:77//Z96802  
 R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPC14-793P23 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//1.1e-62:539:79//AC006208  
 40 R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//1.2e-36:285:83//  
 AC003665  
 R-HEMBA1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-  
 51:416:79//AC004820  
 R-HEMBA1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs  
 and polymorphic CA repeat.//3.9e-18:211:79//Z95113  
 45 R-HEMBA1000025//HS\_3064\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765  
 R-HEMBA1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein  
 family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete  
 50 sequence.//1.5e-32:452:70//Z85986  
 R-HEMBA1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey se-  
 quence.//9.3e-63:541:77//B66264  
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//  
 AF084928  
 55 R-HEMBA1000039//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.4e-44:456:  
 68//AC005291  
 R-HEMBA1000044//Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064  
 R-HEMBA1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-

09:330:63//AC002300

R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM BB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM BB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM BB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM BB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM BB1000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM BB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM BB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM BB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM BB1000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134

R-HEM BB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM BB1000175

R-HEM BB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM BB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM BB1000217

R-HEM BB1000218//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM BB1000266//RPC111-76C20.TV RPC111 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

# EP 1 074 617 A2

R-HEM BB1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

5 R-HEM BB1000284//Homo sapiens full-length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018

R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM BB1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

10 R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

15 R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605

20 R-HEM BB1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681

R-HEM BB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

25 R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644

R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751

R-HEM BB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence.//9.0e-25:179:79//AC004067

30 R-HEM BB10003741//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199

R-HEM BB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675

R-HEM BB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080

35 R-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838

R-HEM BB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

40 R-HEM BB1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251

R-HEM BB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053

R-HEM BB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069

45 R-HEM BB1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700

R-HEM BB1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207

50 R-HEM BB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920

R-HEM BB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007

R-HEM BB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

55 R-HEM BB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849

R-HEM BB1000487

- R-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423
- R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023
- 5 R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721
- 10 R-HEM BB1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397
- R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477
- R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079
- 15 R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//4.2e-74:428:92//AC006236
- R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321
- 20 R-HEM BB1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824
- R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786
- R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914
- 25 R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405
- R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//7.2e-52:260:80//AC003695
- R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280
- 30 R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//1.3e-14:409:65//AC005208
- R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184
- R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831
- 35 R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381
- R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717
- 40 R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724
- R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058
- R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176
- 45 R-HEM BB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085
- R-HEM BB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112
- R-HEM BB1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993
- 50 R-HEM BB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061
- R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031
- 55 R-HEM BB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence.//0.98:251:63//AB005247
- R-HEM BB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chro-

mosome X.//6.8e-58:296:85//Z83313  
 R-HEM BB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731  
 R-HEM BB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584  
 5 R-HEM BB1000705//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723  
 R-HEM BB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943  
 R-HEM BB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380  
 10 R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374  
 R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066  
 15 R-HEM BB1000726//Homo sapiens PAC clone DJ1185107 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990  
 R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875  
 R-HEM BB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069  
 20 R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071  
 R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205  
 25 R-HEM BB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046  
 R-HEM BB1000789//RPCI11-2114.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2114, genomic survey sequence.//3.0e-09:299:64//B63628  
 R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740  
 30 R-HEM BB1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291  
 R-HEM BB1000807  
 R-HEM BB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542  
 35 R-HEM BB1000821  
 R-HEM BB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944  
 R-HEM BB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043  
 40 R-HEM BB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017  
 R-HEM BB1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850  
 R-HEM BB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368  
 45 R-HEM BB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283  
 R-HEM BB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086  
 50 R-HEM BB1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816  
 R-HEM BB1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523  
 55 R-HEM BB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474  
 R-HEM BB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//



AC005621

R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061

R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

5 R-HEM BB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM BB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

10 R-HEM BB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEM BB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024

R-HEM BB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037

15 R-HEM BB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739

R-HEM BB1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015

R-HEM BB1000927

20 R-HEM BB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228

R-HEM BB1000959//Homo sapiens chromosome 17, clone HRC905N1, complete sequence.//5.7e-89:544:90//AC003098

25 R-HEM BB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//0.038:377:58//AC005560

R-HEM BB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234

R-HEM BB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443

30 R-HEM BB1000985//HS\_3184\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008

R-HEM BB1000991

R-HEM BB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368

35 R-HEM BB1001004

R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056

R-HEM BB1001011//HS\_3017\_B1\_G03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944

40 R-HEM BB1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549

R-HEM BB1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475

45 R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527

R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699

R-HEM BB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586

50 R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014

R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187

55 R-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973

R-HEM BB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375

R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

- R-HEM BB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735
- R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
- 5 R-HEM BB1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
- R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570
- 10 R-HEM BB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113
- R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
- 15 R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
- R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077
- R-HEM BB1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
- 20 R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
- R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
- 25 R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
- R-nnnnnnnnnnnr//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
- R-HEM BB1001177
- 30 R-HEM BB1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226
- R-HEM BB1001199
- R-HEM BB1001208
- R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
- 35 R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199
- R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
- 40 R-HEM BB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950
- R-HEM BB1001234
- R-HEM BB1001242
- R-HEM BB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377
- 45 R-HEM BB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089
- R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
- R-HEM BB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
- 50 R-HEM BB1001271//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544
- 55 R-HEM BB1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
- R-HEM BB1001288
- R-HEM BB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-

31:301:78//AC005601  
R-HEM BB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//  
AC003083  
R-HEM BB1001302  
5 R-HEM BB1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE.//6.3e-15:396:64//AL033397  
R-HEM BB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//  
3.4e-42:293:86//AG013777  
R-HEM BB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511  
10 R-HEM BB1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//2.3e-39:301:  
82//AC004585  
R-HEM BB1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096  
R-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//  
15 0.037:103:77//D63850  
R-HEM BB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete  
sequence.//9.1e-19:229:77//AC003037  
R-HEM BB1001337  
R-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056  
20 R-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mi-  
tochondrial protein, complete cds.//2.7e-59:292:99//AF097441  
R-HEM BB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//  
9.1e-41:326:82//AC004859  
R-HEM BB1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING  
25 DRAFT SEQUENCE.//1.8e-11:213:67//Z82207  
R-HEM BB1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940  
R-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete se-  
quence.//4.1e-37:419:73//AC005876  
30 R-HEM BB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:  
75//U91326  
R-HEM BB1001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING  
DRAFT SEQUENCE.//1.8e-28:224:83//AL021686  
R-HEM BB1001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
35 nomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896  
R-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//  
AF071314  
R-HEM BB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:  
63//AC003953  
40 R-HEM BB1001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//1.4e-55:494:  
76//AC005549  
R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:  
63//AC006204  
R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//  
45 AC002370  
R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library)  
complete sequence.//1.3e-46:328:84//AC002350  
R-HEM BB1001429//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160  
50 R-HEM BB1001436  
R-HEM BB1001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934  
R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
2.7e-23:339:69//AC005522  
55 R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:  
299:84//AC005355  
R-HEM BB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:  
486:59//AE001430

- R-HEM BB1001463//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154
- R-HEM BB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941
- 5 R-HEM BB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762
- R-HEM BB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
- R-HEM BB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642
- 10 R-HEM BB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000
- R-HEM BB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070
- R-HEM BB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581
- 15 R-HEM BB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169
- R-HEM BB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394
- R-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049
- R-HEM BB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267:88//AC002301
- 20 R-HEM BB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225
- R-HEM BB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840
- 25 R-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677
- R-HEM BB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236
- R-HEM BB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106
- 30 R-HEM BB1001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302:59//AL010235
- R-HEM BB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503:68//Z93023
- 35 R-HEM BB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368
- R-HEM BB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062
- 40 R-HEM BB1001635//Homo Sapiens Chromosome X clone bW XD90, complete sequence.//1.5e-23:407:69//AC004075
- R-HEM BB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368
- R-HEM BB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506
- 45 R-HEM BB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344
- R-HEM BB1001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572
- R-HEM BB1001668
- 50 R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546
- R-HEM BB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429
- R-HEM BB1001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:31:83//AC005411
- R-HEM BB1001695
- 55 R-HEM BB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704
- R-HEM BB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851

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R-HEM BB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020

R-HEM BB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992

5 R-HEM BB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613

R-HEM BB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221

10 R-HEM BB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671

R-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829

R-HEM BB1001753//RPC111-59J22.TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046

15 R-HEM BB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130

R-HEM BB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050

20 R-HEM BB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157

R-HEM BB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170

25 R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140

R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391

30 R-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882

R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996

R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209

35 R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328

R-HEM BB1001839

R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241

40 R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436

R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327

R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754

45 R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553

R-HEM BB1001872//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027

R-HEM BB1001874

50 R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272

R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//1.3e-49:461:77//AC005922

R-HEM BB1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858

55 R-HEM BB1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345

R-HEM BB1001906

R-HEM BB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

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R-HEM BB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070

R-HEM BB1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929

5 R-HEM BB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417

R-HEM BB1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422

R-HEM BB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099

10 R-HEM BB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406

R-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//8.3e-12:202:69//AB020867

R-HEM BB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544

15 R-HEM BB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408

R-HEM BB1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335

R-HEM BB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846

20 R-HEM BB1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676

R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037

R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077

25 R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736

R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675

R-HEM BB1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617

30 R-HEM BB1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417

R-HEM BB1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420

35 R-HEM BB1001990//Homo sapiens full-length insert cDNA clone ZC33G03.//7.8e-95:456:99//AF086192

R-HEM BB1001996

R-HEM BB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055

R-HEM BB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816

40 R-HEM BB1002005//Homo sapiens chromosome 3p clone RPC15-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903

R-HEM BB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904

R-HEM BB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336

45 R-HEM BB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389

R-HEM BB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612

50 R-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740

R-HEM BB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778

R-HEM BB1002049//Human Chromosome X clone bWXD187, complete sequence.1/1.9e-21:384:64//AC004383

55 R-HEM BB1002050//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//2.5e-37:368:76//AC005553

R-HEM BB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782

R-HEM BB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799

R-HEM BB1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//3.8e-45:307:87//AC005828

5 R-HEM BB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943

R-HEM BB1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279

R-HEM BB1002139//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573

10 R-HEM BB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006

R-HEM BB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881

R-HEM BB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385

15 R-HEM BB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913

R-HEM BB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846

R-HEM BB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148

R-HEM BB1002218//, complete sequence.//3.4e-17:178:82//AC005300

20 R-HEM BB1002232//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599

R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//2.9e-13:227:70//AC005829

R-HEM BB1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

25 R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

R-HEM BB1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

30 R-HEM BB1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216

R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534

R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642

35 R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129

R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028

R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313

40 R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849

R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841

45 R-HEM BB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366

R-HEM BB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038

R-HEM BB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036

50 R-HEM BB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094

R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467

R-HEM BB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182

55 R-HEM BB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091

R-HEM BB1002415//Homo sapiens chromosome 17, clone hRPK.209\_D\_14, complete sequence.//1.4e-25:202:

79//AC005730  
R-HEM BB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//  
AC004799  
R-HEM BB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046  
5 R-HEM BB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING  
DRAFT SEQUENCE.//1.4e-115:557:98//AL034349  
R-HEM BB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS  
and GSSs, complete sequence.//6.3e-37:338:80//AL031012  
R-HEM BB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of  
10 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659  
R-HEM BB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAI project).//0.42:110:  
74//AL021635  
R-HEM BB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302  
R-HEM BB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey se-  
15 quence.//3.1e-14:410:63//AQ238960  
R-HEM BB1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762  
R-HEM BB1002502//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//9.6e-81:538:  
86//AC006120  
20 R-HEM BB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Trans-  
lation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete  
sequence.//0.0061:482:57//AL031313  
R-HEM BB1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309  
25 R-HEM BB1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE.//2.0e-62:201:85//AL033397  
R-HEM BB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:  
58//AC004225  
R-HEM BB1002531  
30 R-HEM BB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15,  
WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009  
R-HEM BB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey se-  
quence.//3.5e-12:414:63//B63283  
R-HEM BB1002550  
35 R-HEM BB1002556//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14;  
HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160  
R-HEM BB1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORK-  
ING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422  
R-HEM BB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968  
40 R-HEM BB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163  
R-HEM BB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING  
DRAFT SEQUENCE.//8.5e-44:335:83//AL021707  
R-HEM BB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC  
Library) complete sequence.//2.0e-105:470:96//AC005865  
45 R-HEM BB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//  
AC004223  
R-HEM BB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//  
AC006162  
R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey se-  
50 quence.//1.1e-44:234:98//AQ060197  
R-HEM BB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:  
65//U91321  
R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC  
Library) complete sequence.//3.0e-72:302:85//AC005908  
55 R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
brary) complete sequence.//3.8e-10:512:60//AC004801  
R-HEM BB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-  
24:486:63//AC005520



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R-HEM BB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953

R-HEM BB1002635//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910

5 R-HEM BB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090

R-HEM BB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694

10 R-HEM BB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090

R-HEM BB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//1.7e-18:504:62//AC002430

R-HEM BB1002686//Homo sapiens full-length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217

R-HEM BB1002692//Homo sapiens 12p13.3 BAC RPC11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206

15 R-HEM BB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153

R-HEM BB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511

R-HEM BB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence.//8.6e-43:351:8011859764

20 R-HEM BB1002705//Plasmodium yoelii rhoptry protein, complete cds.//0.0064:454:59//L27838

R-HEM BB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052

R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037

25 R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720

R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163

30 R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058

R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090

35 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054

R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicro1.//0.79:63:77//AF025889

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366

40 R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867

50 R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//3.4e-39:297:85//AC003976

55 R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641

R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882

R-MAMMA1000133

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

5 R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and puta-

10 tive CpG islands, complete sequence.//2.1e-68:562:78//AL022476

R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381

15 R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic MseI fragment, clone 186c5, reverse read cpg186c5.rt1b.//0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552

20 R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667

R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728

25 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266

30 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-

35 ING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

40 QUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656

R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549

45 R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722

50 R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.1e-16:169:77//AC005553

R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795

55 R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00020:384:60//AF029779

R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence.//0.0026:310:60//AF003518

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R-MAMMA1000313//Human cosmid Xq28\_IA649, complete sequence.//1.5e-26:317:67//U82694  
R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
3.1e-39:277:86//AC004947  
R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180:89//AF015147  
5 R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.97:  
293:64//AE001388  
R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72//U85195  
R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.73:  
332:61//AC002493  
10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//4.6e-80:279:89//  
AC005189  
R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING  
DRAFT SEQUENCE.//7.8e-18:346:63//AL031676  
R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
15 ING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344  
R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING  
DRAFT SEQUENCE.//1.0e-28:225:84//AL031658  
R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey se-  
quence.//4.7e-60:298:99//AQ038102  
20 R-MAMMA1000395  
R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence.//1.4e-84:276:88//  
AC004692  
R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//6.7e-35:360:  
76//AC002394  
25 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//3.1e-69:327:  
79//AC004662  
R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains  
GSS (BAC end sequence),STS.//3.6e-41:180:87//AL009028  
R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
30 3.1e-59:478:77//AC005377  
R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence.//5.3e-53:294:82//X58139  
R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING  
DRAFT SEQUENCE.//1.0:252:59//AL031737  
R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-50:491:76//AC004816  
35 R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950  
R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484  
R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
2.0e-58:564:77//AC004821  
40 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83//  
AC002067  
R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672  
R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//  
0.99:182:61//AB019236  
45 R-MAMMA1000468  
R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.//  
1.0e-38:142:88//AG010148  
R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING  
DRAFT SEQUENCE.//1.3e-37:286:83//Z93015  
50 R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
quence.//4.3e-34:158:86//B54637  
R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90//  
AC006130  
55 R-MAMMA1000500//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.2e-41:  
334:79//L78833  
R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORK-  
ING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118  
R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING

DRAFT SEQUENCE.//1.3e-43:318:83//Z82207  
R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289  
R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING  
5 DRAFT SEQUENCE.//2.2e-30:245:83//Z93015  
R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205  
R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419  
R-MAMMA1000576  
10 R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//5.4e-53:297:85//AC005666  
R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018  
R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT  
15 SEQUENCE.//4.3e-26:293:75//AJ009613  
R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131  
R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956  
20 R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364  
R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970  
R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573  
25 R-MAMMA1000623  
R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498  
R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39B17, WORKING  
DRAFT SEQUENCE.//1.4e-06:236:68//AL023656  
30 R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555  
R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578  
35 R-MAMMA1000670  
R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785  
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623  
R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387  
40 R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075  
R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478  
45 R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694  
R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366  
50 R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781  
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163  
55 R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077  
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.4e-14:309:68//AC004832

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R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722

R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507

5 R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115

R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence.//0.095:367:60//B20150

R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661

10 R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178

R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169

15 R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454

20 R-MAMMA1000778//Human DNA sequence from 4PTTEL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120

R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042

25 R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807

30 R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726\_O\_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323

35 R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985

R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815

R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744

40 R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461

45 R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364

50 R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301

R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653

55 R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658

R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains

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ESTs STS and CpG island.//3.2e-34:354:75//Z93023  
R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425  
R-MAMMA1000883  
5 R-MAMMA1000897  
R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506  
R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110  
10 R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024  
R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247  
R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379  
15 R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777  
R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046  
20 R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347  
R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383  
R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477  
25 R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559  
R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096  
R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001  
30 R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263  
R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152  
35 R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930  
R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219  
R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190  
40 R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101  
R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929  
45 R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910  
R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913  
R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074  
50 R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285  
R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089  
R-nnnnnnnnnnnnn  
55 R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394  
R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326  
R-MAMMA1001073  
5 R-MAMMA1001074//Homo sapiens BAC clone NH0400O10 from Y, complete sequence.//8.6e-33:457:69//AC006040  
R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605  
R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609  
10 R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403  
R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499  
R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-51:267:82//AC005951  
15 R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//6.9e-22:178:85//Z99570  
R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPK1169K15, complete sequence.//3.0e-19:141:81//AC003963  
R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109  
20 R-MAMMA1001133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847  
R-MAMMA1001139//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345  
25 R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684  
R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//9.5e-49:512:74//AC005922  
R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289  
30 R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286  
R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651  
R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387  
35 R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125  
R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662  
40 R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156  
R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748  
R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412  
45 R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:442:61//AC004763  
R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393  
R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708  
50 R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762  
R-MAMMA1001243  
R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo-sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862  
55 R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221  
R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115  
R-MAMMA1001259  
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

# EP 1 074 617 A2

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

5 R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

10 R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.5e-38:306:83//AC005703

15 R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

20 R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

25 R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041

30 R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685

R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

R-MAMMA1001388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707

35 R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044

R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805

40 R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928

R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957

45 R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179

R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126

R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047

50 R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491

R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//AL024493

55 R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295

R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783

R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108\_L\_11, complete sequence.//5.1e-30:286:79//AC005206



R-MAMMA1001501  
R-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714  
R-MAMMA1001510  
5 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352  
R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418  
R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997  
10 R-MAMMA1001575  
R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764  
R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027  
R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216  
15 R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238  
20 R-MAMMA1001606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985  
R-MAMMA1001620//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650  
R-MAMMA1001627//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090  
25 R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399  
R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.2e-21:241:70//AC005386  
R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466  
30 R-MAMMA1001649  
R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811  
R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216  
35 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614  
R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393  
R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166  
40 R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261  
R-MAMMA1001692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345  
45 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324  
R-MAMMA1001715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330  
R-MAMMA1001730  
50 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:382:63//X60786  
R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050  
R-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//4.0e-108:566:95//AC006017  
55 R-MAMMA1001744  
R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//3.5e-113:564:97//AF070718  
R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence.//3.6e-30:312:75//

AC005625  
R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//  
4.7e-34:320:77//AF041338  
5 R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4\_G\_17, complete sequence.//4.7e-10:244:67//  
AC003688  
R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38L16, genomic survey  
sequence.//1.3e-10:236:64//AQ029432  
R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60//AC005140  
10 R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//1.6e-42:416:  
76//AC005332  
R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.4e-13:129:  
83//AC004686  
R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991  
15 R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 un-  
ordered pieces.//1.1e-42:282:85//AC000360  
R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:  
282:86//U91319  
R-MAMMA1001788  
20 R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
9.8e-43:530:71//AC004913  
R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-  
43:324:79//AC004020  
R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:  
25 183:63//AE001432  
R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
1.1e-10:417:62//AC005018  
R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) com-  
plete sequence.//2.6e-40:313:84//AC005859  
30 R-MAMMA1001818  
R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//  
AC004086  
R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
1.9e-53:291:85//AC004966  
35 R-MAMMA1001836//HS\_3164\_B1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484  
R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
R32804, complete sequence.//8.4e-55:309:85//AC003682  
R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//  
40 AC006144  
R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered piec-  
es.//2.4e-50:516:74//AC002099  
R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-  
38:308:82//AC002425  
45 R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, com-  
plete sequence.//6.5e-50:283:86//U80460  
R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21  
unordered pieces.//3.4e-36:224:86//AC005143  
R-nnnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:  
50 495:63//AE001417  
R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//3.2e-42:446:76//AC003117  
R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN  
(PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKNA1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes.  
55 Contains probable GTPase and receptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996  
R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs,  
tRNA.//1.3e-15:181:76//Z82097  
R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 ~complete genomic se-

quence, complete sequence.//1.7e-43:283:86//AC002303  
 R-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING  
 DRAFT SEQUENCE.//1.4e-48:420:79//AL031720  
 R-nnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373  
 5 R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:  
 63//AF041008  
 R-MAMMA1001956//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//1.4e-51:422:79//AL034380  
 R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149  
 10 R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete se-  
 quence.//8.7e-10:186:76//AC002128  
 R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:  
 86//AC003071  
 R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3  
 15 unordered pieces.//1.8e-44:525:72//AC004581  
 R-MAMMA1002009//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING  
 DRAFT SEQUENCE.//1.4e-43:282:79//AL023879  
 R-MAMMA1002011  
 R-MAMMA1002032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING  
 DRAFT SEQUENCE.//1.1e-39:310:84//AL031284  
 20 R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-  
 17:170:81//AC003954  
 R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865  
 R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:  
 25 80//U91318  
 R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:  
 75//U91318  
 R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506\_H\_21, complete sequence.//6.6e-48:367:  
 82//AC005962  
 30 R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 0.25:139:69//AC005052  
 R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
 pieces.//2.2e-45:406:78//AC004676  
 R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.3e-22:357:  
 35 64//AC005291  
 R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//  
 AC004263  
 R-MAMMA1002084//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1174N9, WORKING  
 DRAFT SEQUENCE.//8.9e-41:319:83//AL031602  
 40 R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey se-  
 quence.//9.7e-17:129:88//B69983  
 R-MAMMA1002108  
 R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete  
 sequence.//0.94:168:64//Z73495  
 45 R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.8e-40:313:83//  
 AC005670  
 R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:  
 83//AC004953  
 R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease  
 50 (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801  
 R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//  
 6.6e-06:130:73//AF027357  
 R-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 DRAFT SEQUENCE.//6.0e-19:242:73//AL031447  
 55 R-MAMMA1002153//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0281M17;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.1e-51:291:75//AC006052  
 R-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 608E8, WORKING  
 DRAFT SEQUENCE.//1.2e-53:461:79//AL022343

- R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997
- R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418
- 5 R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588
- 10 R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871
- R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890
- 15 R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.2e-23:269:74//AC005821
- R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158
- R-MAMMA1002219//Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802
- 20 R-MAMMA1002230//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379
- R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253
- 25 R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//2.8e-119:582:98//AC005666
- R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600
- R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-33:571:67//AC006120
- 30 R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749
- R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey sequence.//4.7e-05:153:69//B15590
- 35 R-MAMMA1002282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987
- R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358
- R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568
- 40 R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-35:281:82//AC004231
- R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375
- R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//.8e-17:296:70//AC005074
- 45 R-MAMMA1002299//HS\_3116\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526
- R-MAMMA1002308
- R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979
- 50 R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210
- R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869
- R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054
- 55 R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756
- R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042

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R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991  
R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//3.4e-46:393:71//AC004973  
5 R-MAMMA1002333//HS\_3245\_A1\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759  
R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549  
R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088  
10 R-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100  
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228  
R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996  
15 R-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241  
R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//8.3e-28:187:91//AC004662  
R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869  
20 R-MAMMA1002360//HS\_2163\_B2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213  
R-MAMMA1002361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520  
25 R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196  
R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168  
R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801  
30 R-MAMMA1002385  
R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430  
R-MAMMA1002411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668  
35 R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146  
R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997  
R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321  
40 R-MAMMA1002428//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423  
R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396  
45 R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387:72//B65379  
R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512  
R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982  
R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556  
50 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822  
R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533:93//AC005077  
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460  
55 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375  
R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859  
R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING

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DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139  
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//  
1.2e-101:529:95//AF065214  
5 R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//  
AF041427  
R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:  
84//AC004056  
R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete  
sequence.//9.6e-13:237:67//AC005878  
10 R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey  
sequence.//9.7e-14:216:73//AQ261427  
R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey  
sequence.//4.6e-25:142:99//AQ279542  
15 R-MAMMA1002573//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 811H13, WORKING  
DRAFT SEQUENCE.//1.1e-30:250:82//AL023805  
R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580  
R-MAMMA1002590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 8d5, forward read cpg8d5.f1g.//  
1.0:114:64//Z63758  
20 R-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING  
DRAFT SEQUENCE.//9.0e-96:459:98//AL034548  
R-MAMMA1002598//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORK-  
ING DRAFTSEQUENCE.//0.79:362:58//AL031847  
R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.3e-46:333:  
80//AC005803  
25 R-MAMMA1002612//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 269M15, WORK-  
ING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395  
R-MAMMA1002617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING  
DRAFT SEQUENCE.//1.7e-20:308:71//AL031594  
R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067  
30 R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598  
R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:  
83//AC004050  
R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171\_L\_10, complete sequence.//2.7e-80:344:  
84//AC004687  
35 R-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING  
DRAFT SEQUENCE.//2.6e-34:391:72//AL031727  
R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmid R32543,, and F15613 con-  
taining ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006  
R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
40 1.1e-52:285:92//AC004895  
R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666  
R-MAMMA1002646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING  
DRAFT SEQUENCE.//2.5e-24:285:68//AL023585  
45 R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:  
237:61//X03424  
R-MAMMA1002655//Homo sapiens mini satellite ceb1 repeat region.//0.18:152:65//AF048727  
R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870  
R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:  
92//Z92844  
50 R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey se-  
quence.//0.99:151:66//AQ194411  
R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the  
OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete  
sequence.//3.1e-38:410:76//AL022162  
55 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987  
R-MAMMA1002685//HS\_2052\_A1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2052 Col=3 Row=O, genomic survey sequence.//1.2e-23:255:75//AQ231087  
R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)

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complete sequence.//1.1e-38:299:83//AC004673  
R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbp1 mRNA, partial cds.//3.3e-05:61:93//  
AF057285  
5 R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399  
R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC li-  
brary) complete sequence.//0.26:365:62//AC005293  
R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995  
R-MAMMA1002721//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
DRAFT SEQUENCE.//2.3e-40:279:87//Z83826  
10 R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710  
R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete se-  
quence.//1.1e-42:410:74//AC002037  
R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//  
15 U96629  
R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//2.2e-108:544:  
97//AC005856  
R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human  
PAC Library) complete sequence.//5.9e-106:551:95//AC006055  
20 R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
1.7e-34:305:79//AC005020  
R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds,  
and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626  
R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//  
25 AC005781  
R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//  
AC006128  
R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chro-  
mosome X.//0.94:260:62//Z82975  
30 R-MAMMA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
DRAFT SEQUENCE.//2.6e-21:529:62//AL031667  
R-MAMMA1002782//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING  
DRAFT SEQUENCE.//2.8e-30:234:72//AL022320  
R-MAMMA1002796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING  
35 DRAFT SEQUENCE.//1.0:155:66//AL021394  
R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs  
and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island,  
complete sequence.//5.0e-42:443:75//Z95331  
R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey se-  
40 quence.//1.3e-14:95:87//B17487  
R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//  
AC002073  
R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC  
Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295  
45 R-MAMMA1002835  
R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585  
R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey  
sequence.//5.2e-43:168:85//B67141  
R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007  
50 R-MAMMA1002844  
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067  
R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
9.6e-39:288:81//AC004906  
R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:  
55 57//AC006044  
R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library)  
complete sequence.//1.3e-09:143:76//AC005296  
R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial

cds for thymopoietin beta.//5.1e-41:264:87//U18271  
R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL022069  
R-MAMMA1002887  
5 R-MAMMA1002890  
3.4e-49:376:81//AG006257  
R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//AC004881  
R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502  
10 R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070  
R-MAMMA1002909//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798  
R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019  
15 R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219  
R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//6.3e-88:556:87//AC006120  
R-MAMMA1002947 -  
20 0.48:156:69//AC005469  
R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997  
R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200  
25 R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt] .//0.97:305:62//S81737  
R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280  
R-MAMMA1002982 1.0e-27:110:85//AG005524  
R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460  
30 R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109  
R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406  
R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109  
35 R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092  
R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740  
R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence.//2.7e-14:294:68//B71583  
40 R-MAMMA1003026//HS\_2166\_B2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639  
R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214  
45 R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550  
R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889  
R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235  
50 R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560  
R-MAMMA1003047  
R-MAMMA1003049  
55 R-MAMMA1003055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//2.3e-45:317:86//Z93783  
R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//AC005305



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R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352  
R-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
DRAFT SEQUENCE.//3.1e-49:299:87//Z83826  
R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//  
5 AC005084  
R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
quence.//4.2e-44:338:82//B71494  
R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:  
423:79//U72634  
10 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE,  
100 unordered pieces.//4.8e-114:567:97//AC006087  
R-MAMMA1003127//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
DRAFT SEQUENCE.//1.4e-34:283:83//Z99716  
R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776  
15 R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//  
AC003663  
R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, com-  
plete cds.//4.8e-08:438:59//M97514  
R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
20 DRAFT SEQUENCE.//1.7e-63:149:94//AL021579  
R-MAMMA1003166//HS\_3128\_A1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766  
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640  
R-NT2RM4000024  
25 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//  
AC004993  
R-NT2RM4000030//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//  
U70653  
R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//  
30 Z26239  
R-NT2RM4000061  
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639  
R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey se-  
quence.//7.2e-18:277:71//B49463  
35 R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//  
Z88817  
R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:  
336:65//AC005199  
R-NT2RM4000155  
40 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//3.4e-23:335:  
72//AC005856  
R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//  
D12646  
R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154  
45 R-NT2RM4000191  
R-NT2RM4000197//HS\_3241\_A2\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812  
R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete se-  
quence.//0.0047:193:63//AC006056  
50 R-NT2RM4000200  
R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:  
334:76//AC004035  
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255  
R-NT2RM4000215  
55 R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
2.1e-55:303:86//AC005383  
R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735  
R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.7e-

49:322:88//AC006116  
R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR Region, complete sequence.//  
0.97:184:66//AC000085  
5 R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055  
R-NT2RM4000290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING  
DRAFT SEQUENCE.//1.4e-05:229:65//AL023585  
R-NT2RM4000324  
R-NT2RM4000327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING  
DRAFT SEQUENCE.//3.3e-42:443:75//Z97199  
10 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
6.4e-64:433:84//AC004826  
R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630  
R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066  
R-NT2RM4000356  
15 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542  
R-NT2RM4000368  
1.6e-48:348:85//AG006257  
R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148  
R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
20 quence.//1.4e-25:207:75//871494  
R-NT2RM4000414//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
DRAFT SEQUENCE.//7.1e-17:492:64//AL031985  
R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence.//  
1.8e-40:311:82//AQ241167  
25 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
QUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867  
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:  
78//AF062476  
R-NT2RM4000457  
30 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952  
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461  
R-NT2RM4000496  
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829  
R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey se-  
35 quence.//1.5e-20:150:89//B95717  
R-nnnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556  
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790  
R-NT2RM4000531  
40 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:  
66//AE001391  
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//  
K00909  
R-NT2RM4000585//HS\_3252\_A2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
45 nomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890  
R-NT2RM4000590//CIT-HSP-539O24.TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey se-  
quence.//1.7e-38:226:93//B50657  
R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072  
R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey se-  
50 quence.//0.77:139:64//AQ051950  
R-nnnnnnnnnnnnn  
R-NT2RM4000616//HS\_3107\_A2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034  
R-NT2RM4000674  
55 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823  
R-NT2RM4000698  
R-nnnnnnnnnnnnn  
R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039

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R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560  
R-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
DRAFT SEQUENCE.//1.0e-107:566:95//AL034379  
5 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303  
R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey se-  
quence.//5.2e-41:244:93//AQ006361  
R-NT2RM4000751//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING  
DRAFT SEQUENCE.//2.7e-28:416:67//AL034405  
10 R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217  
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//  
0.00060:241:62//AC002980  
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2.9e-104:546:94//AB007920  
R-NT2RM4000787//Homo sapiens, clone hRPK.3\_A\_1, complete sequence.//5.3e-32:321:77//AC006198  
15 R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//  
AC005306  
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//  
U58675  
R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF086348  
20 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868  
R-NT2RM4000813  
R-NT2RM4000820//, complete sequence.//2.0e-104:432:97//AC005406  
R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence.//  
2.0e-07:166:68//AB012248  
25 R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013  
R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709  
R-NT2RM4000855  
R-nnnnnnnnnnnn//HS\_3189\_B2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genom-  
ic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597  
30 R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-  
46:207:91//AF077058  
R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.0:336:60//AC002530  
R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12,  
U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete se-  
35 quence.//7.1e-09:259:64//AF011889  
R-NT2RM4000979  
R-NT2RM4000996//HS\_3164\_A1\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3164 Col=3 Row=I, genomic survey sequence.//2.0e-82:443:94//AQ141622  
40 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.2e-112:545:97//AB018272  
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.9e-113:556:97//AB014539  
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:120:82//AJ224639  
R-NT2RM4001047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING  
DRAFT SEQUENCE.//1.0:158:67//AL008733  
45 R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey se-  
quence.//5.8e-19:118:97//AQ004096  
R-nnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//1.0e-05:271:64//  
M10296  
R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey se-  
quence.//1.0:186:63//AQ277294  
50 R-NT2RM4001116  
R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//3.6e-79:468:90//  
AC004593  
R-NT2RM4001151//HS\_2270\_B1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2270 Col=9 Row=J, genomic survey sequence.//5.5e-62:312:98//AQ163739  
55 R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1; WORKING DRAFT SEQUENCE,  
31 unordered pieces.//1.4e-107:536:97//AC005841  
R-NT2RM4001160//HS\_3015\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712

R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201  
 R-NT2RM4001191//HS\_3002\_A1\_F05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791  
 R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857  
 5 R-NT2RM4001203  
 R-NT2RM4001204  
 R-NT2RM4001217  
 R-NT2RM4001256  
 R-NT2RM4001258  
 10 R-NT2RM4001309  
 R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPCI1-71H24 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//0.00055:183:63//AC004551  
 R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117\_K\_16, complete sequence.//4.5e-21:212:79//  
 AC004757  
 15 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey se-  
 quence.//3.8e-30:86:89//AQ021084  
 R-NT2RM4001340  
 0.0027:493:60//AC005133  
 R-NT2RM4001344  
 20 R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey se-  
 quence.//6.5e-16:1.01:99//AQ262797  
 R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey  
 sequence.//0.063:140:65//AQ265776  
 R-NT2RM4001382//HS\_3044\_A1\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668  
 R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000  
 R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920  
 R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete  
 cds.//1.7e-55:235:83//U57391  
 30 R-NT2RM4001412  
 R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library)  
 complete sequence.//1.7e-80:489:89//U69730  
 R-NT2RM4001437//RPCI11-56D2.TJ RPCI11 Homo sapiens genomic clone R-56D2, genomic survey sequence.//  
 3.8e-43:250:93//AQ081969  
 35 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library)  
 complete sequence.//0.0034:224:63//AC005926  
 R-NT2RM4001454//Homo Sapiens Chromosome X clone bWDX90, complete sequence.//2.4e-33:360:68//  
 AC004075  
 R-NT2RM4001455//HS\_3229\_B1\_E04\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289  
 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
 2.2e-51:451:79//AC005282  
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585  
 R-NT2RM4001519//HS\_2208\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 45 nomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836  
 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336  
 R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970  
 R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910  
 50 R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811  
 R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel  
 (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein)  
 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ri-  
 bosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix  
 Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific  
 55 protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core'  
 domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//  
 AL031663

- R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317
- R-nnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942
- R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120
- 5 R-NT2RM4001597//HS\_2059\_A1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136
- R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334
- R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936
- 10 R-NT2RM4001629//RPCI11-54G14.TJ RPCI11 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173
- R-NT2RM4001650
- R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575
- 15 R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685
- R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775
- 20 R-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447
- R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153
- 25 R-nnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430
- R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527
- R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123
- R-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709
- 30 R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483
- R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.9e-18:202:78//Z83868
- R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270
- R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence.//4.4e-106:551:95//AC006017
- 35 R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099
- R-NT2RM4001813
- R-NT2RM4001823
- R-NT2RM4001828//HS\_3073\_A2\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=L, genomic survey sequence.//1.6e-46:255:96//AQ121030
- 40 R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024
- R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184
- R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077
- 45 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633
- R-nnnnnnnnnnn//Hs\_3244\_B1\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798
- R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5.0e-119:592:97//Y17711
- R-NT2RM4001876//Megastigmus wachtlii dinucleotide microsatellite, clone
- 50 MWA47CT.//0.13:134:64//AJ001069
- R-NT2RM4001880
- R-NT2RM4001905//HS\_2016\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877
- 55 R-NT2RM4001922//HS\_2228\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498
- R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34\_M\_24, complete sequence.//0.26:325:63//AC004562
- R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//2.9e-85:421:

98//AC005207  
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162  
 R-NT2RM4001953//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
 DRAFT SEQUENCE.//1.3e-08:175:70//Z83826  
 5 R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey se-  
 quence.//5.7e-69:532:81//B55044  
 R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330  
 R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241  
 R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161  
 10 R-NT2RM4001987  
 R-NT2RM4002013  
 R-NT2RM4002018  
 R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-  
 42:277:89//AC005353  
 15 R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//  
 AC006204  
 R-NT2RM4002054  
 R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659  
 R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//  
 20 U82267  
 R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742  
 R-NT2RM4002067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING  
 DRAFT SEQUENCE.//7.7e-64:476:81//Z97832  
 R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758  
 25 R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504  
 R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered  
 pieces.//9.4e-07:322:62//AC000383  
 R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//  
 30 D12646  
 R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000  
 R-NT2RM4002140  
 R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247  
 R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562  
 35 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535  
 R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//8.0e-43:302:85//  
 AC005696  
 R-NT2RM4002189  
 R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960  
 40 R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344  
 R-NT2RM4002213  
 R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//  
 AC004448  
 R-NT2RM4002251  
 45 R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//  
 AC004837  
 R-NT2RM4002266//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179f11, forward read  
 cpg179f11.ft1a.//0.72:97:69//Z57487  
 R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-  
 50 49:405:84//AC005069  
 R-NT2RM4002281//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING  
 DRAFT SEQUENCE.//1.7e-13:168:77//AL033531  
 R-NT2RM4002287  
 R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered  
 55 pieces.//0.98:208:65//AC004676  
 R-NT2RM4002301//HS\_2028\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262  
 R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-

- gene similar to GPIISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822
- R-nnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317
- 5 R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709
- R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549
- R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417
- 10 R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316
- R-NT2RM4002390
- R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411
- R-NT2RM4002438
- 15 R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008
- R-NT2RM4002452
- R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034
- 20 R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545
- R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255
- 25 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591
- R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882
- R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711
- 30 R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368
- R-nnnnnnnnnnnn
- R-NT2RM4002532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985
- 35 R-NT2RM4002534
- R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271
- R-NT2RM4002571
- R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579
- 40 R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862
- R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422
- 45 R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205
- R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090
- R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098
- 50 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290
- R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749
- R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163
- 55 R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758
- R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//6.0e-10:137:79//D42148

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R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754

R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372

5 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97+++F050079

R-NT2RP2000079//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338

10 R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048

R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873

R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015

R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973

15 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356

R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909

R-nnnnnnnnnnnnn

R-nnnnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827

20 R-NT2RP2000147

R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626

R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924

25 R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728

R-NT2RP2000175

R-NT2RP2000183

30 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//4.3e-39:306:83//AC005325

R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382

35 R-NT2RP2000232

R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401

R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066

40 R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726

R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894

R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077

45 R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179

50 R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409

R-NT2RP2000288

R-NT2RP2000289

R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165

55 R-NT2RP2000298

R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE



pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398

R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039

R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993

R-NT2RP2000414//Mouse DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828

R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.99:150:62//AC005324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142:90//AF102265

R-NT2RP2000438//RPC111-62I13.TK RPC111 Homo sapiens genomic clone R-62I13, genomic survey sequence.//3.1e-06:103:79//AQ199572

R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.0e-22:276:73//AC004691

R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//853940

R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234

R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48:201:64//D10170

R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07:472:59//AF033929

R-nnnnnnnnnnnnn

R-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318

R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.6e-29:167:97//AB005543

R-NT2RP2000617

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514

R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796

R-NT2RP2000668

R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590

R-NT2RP2000764

R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002

R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey se-

quence.//9.5e-32:176:97//B99575  
 R-nnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init. region.//0.0077:418:57//K00916  
 R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//  
 AL011013  
 5 R-NT2RP2000819  
 R-NT2RP2000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 43408, WORKING  
 DRAFT SEQUENCE.//0.00012:181:70//AL033504  
 R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor  
 cell line, partial sequence.//3.7e-27:388:72//U13370  
 10 R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//0.0022:200:  
 68//AC005703  
 R-NT2RP2000863  
 R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412  
 R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer , segment 7/10.//  
 15 0.0028:221:62//AB020875  
 R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266  
 R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336  
 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298  
 R-NT2RP2000965  
 20 R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs,  
 STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393  
 R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.4e-93:484:  
 95//AC005277  
 R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:  
 25 318:62//AE001372  
 R-NT2RP2001036//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING  
 DRAFT SEQUENCE.//2.0e-24:273:73//AL031732  
 R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140  
 30 R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029  
 R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey se-  
 quence.//0.13:97:72//AQ265973  
 R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds,  
 mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete se-  
 35 quence.//0.018:373:57//U61140  
 R-NT2RP2001119  
 R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348  
 R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the  
 TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase  
 40 Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a  
 probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted  
 CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394  
 R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838  
 R-NT2RP2001168  
 45 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949  
 R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey se-  
 quence.//1.3e-33:204:93//B89680  
 R-NT2RP2001196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-65, complete  
 sequence.//1.7e-06:413:61//AL010134  
 50 R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,  
 GSS, complete sequence.//8.5e-15:278:68//AL022153  
 R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudog-  
 ene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete  
 sequence.//0.0020:462:57//AL030995  
 55 R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey se-  
 quence.//8.0e-108:547:96//AQ081110  
 R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein  
 gene, 5' end.//0.0052:350:58//M76713

- R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353
- R-NT2RP2001277//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870
- 5 R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709
- R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//AC006041
- R-NT2RP2001312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520
- 10 R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212
- R-NT2RP2001328//HS\_2213\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874
- R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560
- R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404
- 15 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433
- R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//L19301
- R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z93242
- 20 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294
- R-NT2RP2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108D11, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419
- R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence.//0.94:287:59//U73643
- 25 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702
- R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//D17447
- R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC004801
- 30 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.1e-08:218:67//AC004846
- R-NT2RP2001450
- R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//3.8e-31:254:83//AC002465
- 35 R-NT2RP2001506//C.barati p-47, ntnh, bonT genes.//1.2e-06:415:60//Y12091
- R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559
- R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.1e-104:545:95//Y14494
- R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.0e-16:283:68//AC004596
- 40 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108:96//AF037222
- R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//0.052:112:66//B73597
- R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence.//6.0e-78:383:98//AQ042029
- 45 R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322
- R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407
- R-NT2RP2001597//HS\_3016\_B2\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854
- 50 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.015:445:58//AC006079
- R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:413:63//AF009326
- R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626
- 55 R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125
- R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//

AC004472

R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107:66//AC002385

R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758

5 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352:97//AC004079

R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914

10 R-NT2RP2001740//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104

R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583

R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435:97//AC004783

15 R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9//0.031:261:60//M23468

R-NT2RP2001861

R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//I34189

R-NT2RP2001876

20 R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.0e-111:485:97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563

25 R-NT2RP2001926//HS\_3180\_B2\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504

R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280

R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033

30 R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575

35 R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAll project).//0.031:282:61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715

R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389:61//D88270

40 R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429:61//AC004011

R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239:62//X83707

45 R-NT2RP2002058//HS\_2183\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792

R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183

50 R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STs, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178

55 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191:64//AQ266779

- R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.0065:294:61//AC005913
- R-NT2RP2002154
- 5 R-NT2RP2002172//RPC11-90C20.TJ RPC11 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591
- R-NT2RP2002185//CIT-HSP-2341115.TF CIT-HSP Homo sapiens genomic clone 2341115, genomic survey sequence.//6.0e-36:230:90//AQ053355
- R-NT2RP2002192//HS\_2222\_B1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491
- 10 R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872
- R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785
- R-NT2RP2002219//HS\_2058\_A1\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380
- 15 R-NT2RP2002231//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557
- R-nnnnnnnnnnnn//Sequence 11 from patent US 5624818.//3.3e-91:553:87//I41141
- R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e14:132:84//AF005418
- R-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527
- 20 R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.1e-06:391:60//AC004605
- R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226
- R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532
- 25 R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389:59//AE001408
- R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093668
- 30 R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323:73//L23204
- R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958
- R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308
- 35 R-NT2RP2002408//HS\_2212\_A1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence.//9.6e-35:231:88//AQ184632
- R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877
- 40 R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225
- R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z99289
- 45 R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013
- R-NT2RP2002475
- R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289
- 50 R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047
- R-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.0e-86:429:98//AC006213
- R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334
- 55 R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//0.14:406:58//AJ223323
- R-NT2RP2002537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

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R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314  
R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316  
R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878  
5 R-NT2RP2002595  
R-NT2RP2002606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529  
R-NT2RP2002609  
R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551  
10 R-NT2RP2002621//Human DNA sequence from PAC 341110 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs.//1.1e-38:348:78//Z97352  
R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030  
R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384  
15 R-NT2RP2002701  
R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778  
R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983  
20 R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815  
R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138  
R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674  
25 R-NT2RP2002741//HS\_3051\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283  
R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395  
R-NT2RP2002752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494  
30 R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882  
R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917  
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537  
35 R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850  
R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078  
R-NT2RP2002857//HS\_3026\_B2\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ 128697  
40 R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//1.5e-44:270:85//AQ052700  
R-NT2RP2002880//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318  
45 R-NT2RP2002891  
R-NT2RP2002925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395  
R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556  
R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140  
50 R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//1.0:275:61//AC005701  
R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483  
55 R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132  
R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140

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R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542

R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//1.3e-51:283:88//AC005968

5 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21://4.3e-11:430:63//AL021307

R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887

R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870

10 R-NT2RP2003073

R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914

R-NT2RP2003108

R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378

15 R-NT2RP2003121//HS\_2238\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058

R-NT2RP2003125

R-NT2RP2003129

R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084

20 R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879

R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581

R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018\_N\_14, complete sequence.//2.2e-71:467:86//AC005823

25 R-NT2RP2003177

R-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597

R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877

R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551

30 R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888

R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738

R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481

35 R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525

R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831

40 R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261

R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079

45 R-NT2RP2003295//HS\_2053\_B1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251

R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332

R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960

50 R-NT2RP2003329//C.reinhardtii psbB 5' flanking region.//0.79:161:59//X59731

R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039

R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357

55 R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321

R-NT2RP2003391//HS\_2255\_B2\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937  
 R-NT2RP2003393//RPC11-44K6.TJ RPC11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 3.9e-31:290:79//AQ202481  
 5 R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//  
 X14910  
 R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, par-  
 tial cds.//0.32:174:66//U81429  
 R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536  
 R-NT2RP2003445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 10 DRAFT SEQUENCE.//4.4e-99:585:89//AL023808  
 R-NT2RP2003446  
 R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559  
 R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540  
 R-NT2RP2003499  
 15 R-NT2RP2003506  
 R-NT2RP2003511  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460  
 R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:  
 518:79//M12783  
 20 R-NT2RP2003522//HS\_2182\_A1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304  
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE,  
 31 unordered pieces.//1.5e-37:328:80//AC005841  
 R-NT2RP2003543//HS\_3028\_A2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957  
 R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055  
 R-NT2RP2003564  
 R-NT2RP2003581  
 R-NT2RP2003596//HS\_2163\_B1\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 30 nomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143  
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067  
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507  
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//  
 35 AJ006215  
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chro-  
 mosome X contains ESTs.//0.0053:395:58//Z76735  
 R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385  
 R-NT2RP2003691//HS\_3252\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783  
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey se-  
 quence.//3.9e-43:431:75//AQ035000  
 R-NT2RP2003704  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097  
 45 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X \*.//0.64:169:67//Z84470  
 R-NT2RP2003714//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//  
 4.6e-11:152:73//295704  
 R-nnnnnnnnnnnn/H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631  
 R-NT2RP2003737//Homo sapiens clone DJ102214, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 50 2.2e-109:547:96//AC004951  
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-  
 109:545:97//AC004626  
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019  
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468  
 55 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete  
 cds.//0.96:446:58//D87956  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437  
 R-NT2RP2003777



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R-NT2RP2003781//HS\_3109\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749  
R-NT2RP2003793  
R-NT2RP2003840  
5 R-NT2RP2003857//HS\_2205\_A2\_H12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299  
R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850  
10 R-NT2RP2003871//HS\_3210\_A1\_C08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028  
R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214  
R-NT2RP2003912//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693  
15 R-NT2RP2003952  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916  
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347  
20 R-NT2RP2003984  
R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC0003 82  
R-NT2RP2003988  
R-NT2RP2004014  
25 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780  
R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389  
R-NT2RP2004043//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555  
30 R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308  
R-NT2RP2004098//H.sapiens CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpg133h3.rt1a.//7.9e-25:140:100//Z64530  
35 R-NT2RP2004124  
R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964  
R-NT2RP2004152//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776  
40 R-NT2RP2004165//Anthracidaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021  
R-NT2RP2004170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064  
R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047  
45 R-NT2RP2004187//RPCI11-59E12.TK RPCI11 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120  
R-NT2RP2004194  
R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601  
50 R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//0.19:175:64//AC005023  
R-NT2RP2004226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808  
55 R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524  
R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280

5 R-NT2RP2004270//Lycopersicon esculentum Idh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662

10 R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPC11-90N11.TJ RPC11 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548

15 R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433

20 R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

25 R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164

30 R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS\_3238\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514

35 R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

40 R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591

R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547

R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890

45 R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184

50 R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976

55 R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605

R-NT2RP2004600//Homo sapiens full-length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522

R-NT2RP2004602//Homo sapiens full-length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033

R-NT2RP2004614  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929  
 R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-  
 22:197:79//U63721  
 R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525  
 R-NT2RP2004709//Homo sapiens full-length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259  
 R-NT2RP2004710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 DRAFT SEQUENCE.//6.9e-117:592:96//AL031447  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947  
 R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505  
 R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3.//2.0e-81:568:84//  
 Z97988  
 R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxi-  
 dase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large  
 and small subunits).//4.0e-08:365:62//L04272  
 R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-  
 111:541:98//AC005216  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//  
 2.5e-114:564:96//AF058953  
 R-NT2RP2004802  
 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179  
 R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//4.0e-46:447:72//  
 AC002089  
 R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556  
 R-NT2RP2004897//Human Chromosome X clone bWDX187, complete sequence.//1.1e-08:330:61//AC004383  
 R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey se-  
 quence.//0.99:129:65//AQ110571  
 R-NT2RP2004961//RPCI11-45P2.TK RPCI11 Homo sapiens genomic clone R-45P2, genomic survey sequence.//  
 9.3e-90:453:97//AQ202282  
 R-NT2RP2004962//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H4,  
 WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573  
 R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-  
 52:496:77//AC005077  
 R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//  
 AC005614  
 R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.025:339:61//  
 AC003071  
 R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.//  
 0.40:111:70//B78148  
 R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//  
 0.23:157:68//AC005682  
 R-NT2RP2005000  
 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515  
 R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 complete sequence.//2.4e-21:246:77//AC004673  
 R-NT2RP2005018//HS\_3108\_B1\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050  
 R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//6.6e-41:  
 566:73//U70476  
 R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey se-  
 quence.//4.1e-31:357:75//B49897  
 R-NT2RP2005037

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R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//I25644  
R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475:67//AF009326  
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.4e-104:518:97//AB014564  
5 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//X98743  
R-NT2RP2005139  
R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101  
10 R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911  
R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100:75//AC004971  
R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence.//0.90:113:71//AQ262104  
15 R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence.//5.0e-14:183:75//AC003041  
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5e-100:513:95//AJ007509  
R-NT2RP2005204  
20 R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-119:583:97//AC005189  
R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial.//8.4e-62:312:98//AJ010952  
R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328:62//Z99297  
25 R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355:61//AL034560  
R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541:58//AC000107  
30 R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335  
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.4e-124:594:98//AF060219  
R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590  
R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101  
35 R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//9.5e-15:218:77//AL022069  
R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804  
40 R-NT2RP2005336//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567  
R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.//0.094:451:60//297629  
R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841  
R-NT2RP2005360//Homo sapiens clone RG023115, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266:60//AC005049  
45 R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//6.0e-41:226:86//AC005695  
R-NT2RP2005407  
R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835  
50 R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548  
R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845  
R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2.//2.0e-42:315:82//X71342  
55 R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816  
R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence.//01251288:62//AC005457

- R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510
- 5 R-NT2RP2005476//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746
- R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030
- 10 R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917
- R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051
- R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722
- 15 R-NT2RP2005498
- R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//.7e-29:252:76//AC005828
- 20 R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979
- R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563
- 25 R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432
- R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911
- R-NT2RP2005539//Homo sapiens mRNA for NSI-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449
- R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963
- 30 R-NT2RP2005549//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929
- R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804
- R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//AC004996
- 35 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146
- R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148
- R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126
- 40 R-NT2RP2005620
- R-NT2RP2005622//Jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538
- R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996
- 45 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937
- R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398
- R-NT2RP2005651
- 50 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908
- R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984
- R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814
- 55 R-NT2RP2005683//Jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B13538
- R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478

R-NT2RP2005694//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-106, complete sequence.//0.0026:414:57//AL010210  
R-NT2RP2005701  
5 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342  
R-NT2RP2005719//*Caenorhabditis elegans* cosmid LLC1, complete sequence.//0.83:275:61//Z82277  
R-NT2RP2005722//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985  
R-NT2RP2005723  
10 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842  
R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384  
R-NT2RP2005748//RPC11-64K11.TK RPC11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313  
15 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868  
R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516  
R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098  
20 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672  
R-NT2RP2005773//HS\_2168\_B1\_G12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414  
R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310  
25 R-NT2RP2005781//*Streptomyces* sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623  
R-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423  
R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//6.3e-16:481:63//AC005332  
30 R-NT2RP2005812//*Caenorhabditis elegans* cosmid F15810.//0.81:147:63//AF036696  
R-NT2RP2005815  
R-NT2RP2005835  
R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873  
R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047  
35 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308  
R-NT2RP2005859//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-83, complete sequence.//0.0097:363:59//AL010152  
40 R-NT2RP2005868//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971  
R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316  
R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661  
45 R-NT2RP2005908  
R-NT2RP2005933//*Rattus norvegicus* nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840  
R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289  
50 R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616  
R-NT2RP2006023//HS\_2176\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148  
55 R-NT2RP2006038//*Plasmodium falciparum* chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369  
R-NT2RP2006043//*Polistes annularis* (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835  
R-NT2RP2006052//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING

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DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140  
R-NT2RP2006069  
R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709  
5 R-NT2RP2006098//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-77, complete  
sequence.//4.1e-09:393:62//AL010151  
R-NT2RP2006100//HS\_2020\_A2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761  
10 R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:  
199:79//M85300  
R-NT2RP2006141  
R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:  
76//AC002045  
R-NT2RP2006184//RPCI11-6O16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6O16, genomic survey se-  
15 quence.//0.52:273:61//B49539  
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554  
R-NT2RP2006196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-57, complete  
sequence.//4.2e-05:420:59//AL008981  
R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE,  
20 66 unordered pieces.//2.1e-100:409:96//AC006057  
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484  
R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707  
R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:  
89//U91318  
25 R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//  
AC004008  
R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630  
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262  
R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey se-  
30 quence.//1.2e-27:215:65//B17768  
R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761  
R-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING  
DRAFT SEQUENCE.//2.8e-104:524:96//AL033531  
R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:  
35 78//AC004893  
R-NT2RP2006334  
R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence.//  
2.6e-35:217:92//AQ267043  
R-NT2RP2006393//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
40 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046  
R-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
DRAFT SEQUENCE.//3.2e-42:184:86//AL022345  
R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568  
R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:  
45 60//AE001423  
R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098  
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266  
R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222  
R-NT2RP2006472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING  
50 DRAFT SEQUENCE.//5.4e-12:407:62//AL034386  
R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216  
R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:  
58//AE001370  
R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742  
55 R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//  
AC004660  
R-nnnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532  
R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:

448:64//U22015  
 R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246  
 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972  
 5 R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995  
 R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//1.0:158:66//AC005697  
 10 R-NT2RP3000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522  
 R-NT2RP3000055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378  
 R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192  
 15 R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630  
 R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U-23155  
 R-NT2RP3000109//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776  
 20 R-NT2RP3000134//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746  
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164  
 R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.3e-67:354:95//AC005746  
 25 R-NT2RP3000186  
 R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat.//2.5e-31:295:78//Z82899  
 R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514  
 30 R-NT2RP3000220//RPC111-63O7.TJ RPC111 Homo sapiens genomic clone R-63O7, genomic survey sequence.//0.25:118:66//AQ201832  
 R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063  
 R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530  
 35 R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279  
 R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.025:131:66//AC005726  
 40 R-NT2RP3000252  
 R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879  
 R-NT2RP3000267  
 45 R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766  
 R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970  
 R-NT2RP3000320//HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064  
 R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090  
 50 R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551  
 R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544  
 R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177  
 55 R-NT2RP3000350  
 R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039  
 R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124



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R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634

R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence.//0.015:184:63//B31814

5 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185

R-NT2RP3000418//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510B21, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885

R-NT2RP3000433

R-NT2RP3000439

10 R-NT2RP3000441

R-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K<sup>+</sup> channel protein.//0.71:101:66//E13519

R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889

15 R-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847

R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//I16692

20 R-NT2RP3000512//RPC111-60F15.TK RPC111 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516

R-NT2RP3000526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783

R-NT2RP3000527//HS\_3228\_A1\_H07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence.//4.5e-30:184:93//AQ209131

25 R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538

R-NT2RP3000542//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316

30 R-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.1e-107:548:95//AC006012

R-NT2RP3000562//HS\_2041\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.6e-55:279:98//AQ230207

R-NT2RP3000578//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.00060:356:58//AL010212

35 R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377

40 R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505

R-NNNNNNNNNN//HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452

45 R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128

R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414

50 R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115

R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379

55 R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092

R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//

AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645

R-NT2RP3000685//HS\_3007\_A2\_F02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655

R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

R-NT2RP3000759//HS\_2055\_A2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

R-NT2RP3000836//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.20:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

R-NT2RP3000847//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572

R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153 R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

R-NT2RP3000869//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens/Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.36:186:62//AC006079

R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

R-NT2RP3001007//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

R-NT2RP3001081//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107

- R-nnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316  
 R-NT2RP3001111  
 R-NT2RP3001113
- 5 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189  
 R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.000.13.160:69//AQ002011  
 R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from
- 10 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.9e-99:497:96//AL031864  
 R-NT2RP3001120  
 R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559  
 R-NT2RP3001133
- 15 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305  
 R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448  
 R-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379
- 20 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266  
 R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688  
 R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785  
 R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey
- 25 sequence.//7.0e-29:167:97//B88077  
 R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827  
 R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326
- 30 R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003  
 R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237
- 35 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398  
 R-NT2RP3001253//HS\_3002\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=O, genomic survey sequence.//0.98:190:63//AQ251982  
 R-NT2RP3001260
- 40 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936  
 R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589  
 R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341
- 45 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811  
 R-NT2RP3001307//HS\_2058\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868  
 R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848
- 50 R-NT2RP3001325  
 R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367  
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920  
 R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105
- 55 R-NT2RP3001355  
 R-NT2RP3001374//HS\_2184\_A2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence.//3.7e-10:101:84//AQ024647  
 R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:

- 279:63//AE001397  
 R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785
- 5 R-NT2RP3001392//HS\_3078\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587  
 R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544  
 R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046  
 R-NT2RP3001399
- 10 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160  
 R-NT2RP3001420//Human BAC clone GS165104 from 7q21, complete sequence.//3.7e-29:412:74//AC002379  
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158  
 R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152  
 R-nnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668
- 15 R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029  
 R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903
- 20 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630  
 R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906  
 R-NT2RP3001457  
 R-NT2RP3001459
- 25 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030  
 R-NT2RP3001490//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208  
 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395
- 30 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.1e-110:549:97//AF064801  
 R-NT2RP3001527//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549  
 R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420
- 35 R-NT2RP3001538  
 R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292  
 R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688
- 40 R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337  
 R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//0.066:360:60//AC005410  
 R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490
- 45 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821  
 R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21:31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808
- 50 R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10.//0.99:137:63//X76572  
 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149  
 R-NT2RP3001642
- 55 R-NT2RP3001646//HS\_3218\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003  
 R-NT2RP3001671//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-88, complete sequence.//0.018:262:61//AL010157  
 R-NT2RP3001672

- R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905  
 R-NT2RP3001678//RPC111-50C17.TK RPC111 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359
- 5 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//7.8e-104:549:95//AB020860  
 R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019  
 R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415
- 10 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523  
 R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562  
 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//AC004617
- 15 R-NT2RP3001724//Human HepG2 3' region Mbol cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273  
 R-NT2RP3001730//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200  
 R-NT2RP3001739
- 20 R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279  
 R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378  
 R-NT2RP3001764
- 25 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232  
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928  
 R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262  
 R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962  
 R-NT2RP3001819
- 30 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410  
 R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694  
 R-NT2RP3001855
- 35 R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409  
 R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950  
 R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486
- 40 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142  
 R-NT2RP3001929  
 R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969  
 R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328
- 45 R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500  
 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836  
 R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844
- 50 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029  
 R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987  
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779  
 R-NT2RP3002007
- 55 R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322  
 R-NT2RP3002033  
 R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

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R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877  
R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006  
R-NT2RP3002057  
5 R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002  
R-ntntntntntntntntntnt  
R-NT2RP3002081//HS\_3082\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25 :344:73//AQ122260  
R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
10 plete sequence.//2.6e-23:212:80//AC006210  
R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//  
AC004746  
R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey se-  
quence.//3.5e-08:110:78//AQ059071  
15 R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes,  
complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077  
R-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING  
DRAFT SEQUENCE.//4.1e-108:551:96//AL031710  
R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:  
20 80//AB003503  
R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857  
R-NT2RP3002165  
R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z48711  
R-NT2RP3002173  
25 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980  
R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF100669  
R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs.//0.30:  
217:63//Z82189  
30 R-NT2RP3002255  
R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//0.84:463:57//AF070717  
R-NT2RP3002276//HS\_2260\_A1\_MF\_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491  
R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//  
35 X13546  
R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115  
R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688  
R-NT2RP3002343  
40 R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.20:489:56//AC004617  
R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164  
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578  
R-NT2RP3002484  
R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 con-  
45 tains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359  
R-NT2RP3002512  
R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey se-  
quence.//0.81:266:58//AQ057387  
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272  
50 R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479  
R-NT2RP3002566//HS\_2036\_A1\_D08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627  
R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-  
15:213:73//AC004956  
55 R-NT2RP3002590//Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MXK3, complete sequence.//  
0.00010:431:59//AB019236  
R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522  
R-NT2RP3002603

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R-NT2RP3002631//Homo sapiens chromosome 21 PAC  
 RPCIP704A9190Q2.//1.0:241:59//AJ006997  
 R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//6.8e-24:  
 331:76//M85300  
 5 R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//  
 Z49816  
 R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA,  
 partial sequence.//0.60:300:59//U82072  
 R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704  
 10 R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 4.7e-09:122:77//AQ202481  
 R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276  
 R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037  
 R-NT2RP3002701  
 15 R-NT2RP3002713//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE.//0.95:334:59//AL031427  
 R-NT2RP3002763//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567  
 R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710  
 R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//  
 20 AC004822  
 R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flank-  
 ing repeat regions.//1.1e-20:161:77//AF003528  
 R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972  
 R-NT2RP3002818//HS\_3053\_A2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025  
 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276  
 R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//  
 AC005256  
 R-NT2RP3002876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
 30 DRAFT SEQUENCE.//2.6e-59:311:96//AL034380  
 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//4.6e-24:422:63//AC003035  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314  
 R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//  
 35 AC005014  
 R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500  
 R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:  
 566:96//AC005754  
 R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:  
 40 58//AE001391  
 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666  
 R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482  
 R-NT2RP3002978//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 DRAFT SEQUENCE.//4.8e-05:249:63//AL031733  
 45 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATI-  
 DYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//  
 0.0097:246:67//Z97195  
 R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,  
 G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:  
 50 188:78//AF109905  
 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site.//5.3e-07:376:  
 63//L47211  
 R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-13:323:66//  
 AC005669  
 55 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hll-10).//3.8e-42:  
 265:91//Y16708  
 R-NT2RP3003068//HS\_3214\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013

5 R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153

R-NT2RP3003121//Homo sapiens full-length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348

R-NT2RP3003133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985

10 R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646

R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995

R-NT2RP3003150

15 R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence.//5.5e-42:289:74//AC005294

R-NT2RP3003185//HS\_2058\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298

R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//4.8e-40:349:79//AC005701

20 R-NT2RP3003197//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319

R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904

R-NT2RP3003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183

25 R-NT2RP3003212//Homo sapiens full-length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173

R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307

R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272

30 R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083

R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862

R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022

35 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983

R-NT2RP3003290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662

R-NT2RP3003301

R-NT2RP3003302//CIT-HSP-2319H19.TR CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950

40 R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660

R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287

45 R-NT2RP3003330//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015

R-NT2RP3003344//HS\_3235\_B2\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203

R-NT2RP3003346

50 R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519

R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820

55 R-NT2RP3003385

R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-40:496:



- 72//AL031585  
 R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204  
 R-NT2RP3003411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 438L4, WORKING  
 DRAFT SEQUENCE.//1.0:180:61//Z97635
- 5 R-NT2RP3003427//RPC111-45J23.TJ RPC111 Homo sapiens genomic clone R-45J23, genomic survey se-  
 quence.//0.82:162:69//AQ195566  
 R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:  
 61//AC006031  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//  
 10 AF004828  
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268  
 R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:  
 495:59//AE001398  
 R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene.//0.0074:514:59//X77238
- 15 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(GTG)n repeat-containing mRNA.//1.3e-31:217:88//  
 U00952  
 R-NT2RP3003552  
 R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019  
 R-NT2RP3003564  
 20 R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:  
 59//AL008638  
 R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:  
 79//AC003007  
 R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560
- 25 R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the AD-  
 SL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable  
 rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete  
 sequence.//1.8e-44:448:77//AL022238  
 R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//0.34:257:62//  
 30 AC005291  
 R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701  
 R-NT2RP3003665//HS\_3078\_B2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580  
 R-NT2RP3003672  
 35 R-NT2RP3003686  
 R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//  
 AC002452  
 R-NT2RP3003716//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING  
 DRAFT SEQUENCE.//0.00072:425:62//AL034410
- 40 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300  
 R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-  
 07:217:66//AC003009  
 R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat  
 and GSSs, complete sequence.//8.1e-26:456:68//Z98052
- 45 R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736  
 R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:  
 95//AF077754  
 R-NT2RP3003805  
 50 R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107  
 R-NT2RP3003819//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING  
 DRAFT SEQUENCE.//6.0e-44:288:81//Z84487  
 R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404  
 R-NT2RP3003828
- 55 R-NT2RP3003831//\*\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567  
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611  
 R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-  
 46:457:74//AC002980

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R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-06:356:62//Z98547  
 R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11.//8.2e-09:68:98//AF086402  
 R-NT2RP3003876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORK-  
 ING DRAFT SEQUENCE.//0.0027:180:66//AL031650  
 5 R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array.//0.029:234:62//  
 X53439  
 R-NT2RP3003918  
 R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds.//0.00087:164:  
 67//AF029215  
 10 R-NT2RP3003989  
 R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465  
 R-NT2RP3004013//HS\_3018\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3018 Col=17 Row=M, genomic survey sequence.//0.00026:421:60//AQ119904  
 R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), com-  
 15 plete sequence.//4.8e-12:308:62//AC004532  
 R-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE.//0.42:190:64//AL021579  
 R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//  
 AC006130  
 20 R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308  
 R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//  
 AC005784  
 R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//  
 25 AC002525  
 R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-  
 93:551:92//AC005038  
 R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence.//1.6e-104:317:100//AC006064  
 30 R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2  
 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532  
 R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542  
 R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//  
 0.013:134:70//U78721  
 35 R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//  
 AC004081  
 R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533  
 R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763  
 R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052  
 40 R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498  
 R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:  
 407:60//AE001415  
 R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//  
 2.8e-105:534:97//AC005385  
 45 R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey se-  
 quence.//4.0e-64:382:90//AQ281324  
 R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967  
 R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536  
 R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.4e-06:435:  
 50 62//AC004231  
 R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey se-  
 quence.//0.0018:210:65//AQ263365  
 R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//7.1 e-46:340:83//  
 AC005695  
 55 R-NT2RP3004349//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117O3, WORKING  
 DRAFT SEQUENCE.//9.4e-29:263:79//AL020995  
 R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoam-  
 ine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125

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R-NT2RP3004399//HS\_3046\_A1\_E02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=I, genomic survey sequence.//0.00014:186:67//AQ137619  
R-NT2RP3004424//RPCI11-59114.TJ RPCI11 Homo sapiens genomic clone R-59114, genomic survey sequence.//7.4e-71:370:95//AQ201461

5 R-NT2RP3004428//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282  
R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824  
R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917

10 R-NT2RP3004466  
R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895  
R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504

15 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925  
R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024  
R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982  
R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023

20 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357  
R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260  
R-NT2RP3004507  
R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518

25 R-nnnnnnnnnnnn/Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316  
R-NT2RP3004544  
R-NT2RP3004566  
R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709

30 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083  
R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946  
R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234

35 R-NT2RP3004617  
R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414  
R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679

40 R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749  
R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388  
R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015

45 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266  
R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074  
R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506

50 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648  
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538  
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952  
R-NT2RP4000147

55 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681  
R-NT2RP4000151  
R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439  
R-NT2RP4000167//RPCI11-59L8.TK RPCI11 Homo sapiens genomic clone R-59L8, genomic survey sequence.//

6.2e-26:163:93//AQ200049  
R-NT2RP4000185  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505:96//AB014600  
R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300  
5 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//  
AC005261  
R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//  
AC004081  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470  
10 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092  
R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey se-  
quence.//0.26:124:69//AQ043515  
R-nnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-  
15 squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368  
R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS  
and GSSs, complete sequence.//2.2e-111:538:98//AL033384  
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524  
R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311  
20 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-  
39:350:79//AC004972  
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281  
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//  
8.7e-109:527:98//AF044195  
25 R-NT2RP4000370//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//9.9e-25:348:72//  
AC005154  
R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-  
69:391:89//U17901  
R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//0.066:197:63//  
30 AC006080  
R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey se-  
quence.//0.10:79:75//B15527  
R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313  
R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2  
35 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-  
aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for  
another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete se-  
quence.//1.8e-08:489:59//AL021026  
R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
40 DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505  
R-NT2RP4000449//HS\_2037\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047  
R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271  
R-nnnnnnnnnnnn  
45 R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
clone CSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082  
R-nnnnnnnnnnnn  
R-NT2RP4000500  
R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
50 DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140  
R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:  
77//AC003007  
R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced  
Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseu-  
55 dogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor  
JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068  
R-NT2RP4000519  
R-NT2RP4000524

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R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078

5 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013

10 R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-2300I7.TR CIT-HSP Homo sapiens genomic clone 2300I7, genomic survey sequence.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443

15 R-NT2RP4000704//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080

20 R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669

R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503

25 R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

30 R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098

35 R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

40 R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

45 R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698

R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633O19, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302

50 R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS\_3009\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957

55 R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011TIN.01\_di1PD, partial cds.//0.11:219:62//U44882

R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//I25669

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),

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R-nnnnnnnnnnnr//Homo sapiens full-length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334  
R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:  
466:66//AF009326  
5 R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey se-  
quence.//0.98:305:62//AQ018036  
R-NT2RP4001339  
R-NT2RP4001345  
R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//  
AB003097  
10 R-NT2RP4001353//RPC111-55N17.TJ RPC111 Homo sapiens genomic clone R-55N17, genomic survey se-  
quence.//0.74:106:66//AQ081821  
R-NT2RP4001372  
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//1.5e-09:473:  
60//AC006080  
15 R-NT2RP4001375  
R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey se-  
quence.//9.4e-41:441:75//AQ040083  
R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//  
AC004691  
20 R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140  
R-NT2RP4001414  
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272  
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
25 DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308  
R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220  
R-NT2RP4001474  
R-NT2RP4001483  
30 R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:  
61//L34027  
R-NT2RP4001502//HS\_2187\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108  
R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE,  
35 4 unordered pieces.//0.15:333:62//AC005916  
R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226  
R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086  
R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710  
40 R-nnnnnnnnnnnr//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119  
R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//  
Z82212  
R-NT2RP4001567//RPC111-61A2.TJ RPC111 Homo sapiens genomic clone R-61A2, genomic survey sequence.//  
0.0072:180:60//AQ200771  
45 R-NT2RP4001568  
R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11),  
12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit  
III (COIII) gene, complete cds.//1.6e-09:555:58//U14181  
R-NT2RP4001574//HS\_2247\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
50 nomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345  
R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the  
BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18  
(40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseu-  
dogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6  
55 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type  
XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG  
islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228  
R-NT2RP4001592//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING

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DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

5 R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384

10 R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CiT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380

15 R-NNNNNNNNNN//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735

R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316

20 R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020

R-NT2RP4001803//HS\_3087\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

R-NT2RP4001822

25 R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540

R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

30 R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

35 R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523

40 R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157

R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023

45 R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region.//1.0e-46:242:98//U25276

R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536

50 R-NT2RP4002047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353

55 R-NT2RP4002058//RPCI11-69O1.TJ RPCI11 Homo sapiens genomic clone R-69O1, genomic survey sequence.//0.23:163:64//AQ268418

R-NT2RP4002071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386

R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon



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of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375  
R-NT2RP4002078//RPC111-79I16.TV RPC111 Homo sapiens genomic clone R-79I16, genomic survey sequence.//3.3e-87:452:95//AQ283131  
R-nnnnnnnnnnnnn  
R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619  
R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376O23, genomic survey sequence.//6.8e-62:320:96//AQ111163  
R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476  
R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383  
R-NT2RP4002905//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.0017:533:57//AL008972  
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934  
R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510  
R-OVARC1000006//HS\_2253\_B1\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124  
R-OVARC1000013//HS\_2212\_A2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584  
R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:62//Z80232  
R-OVARC1000017  
R-OVARC1000035//RPC111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194  
R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721  
R-OVARC1000060//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397  
R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276  
R-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387  
R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413  
R-nnnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391  
R-OVARC1000091  
R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520  
R-OVARC 1000106  
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250  
R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342  
R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740  
R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//1.8e-16:370:67//AC005385  
R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492  
R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642  
R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932  
R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506  
R-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604  
R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501  
R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484  
R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63 A 1, complete sequence.//6.2e-38:193:82//

AC005670  
R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194  
5 R-OVARC1000288//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131  
R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//1.7e-10:100:88//AC005971  
R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574  
R-OVARC 1000309  
10 R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236  
R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614  
R-OVARC1000335//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690  
15 R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308  
R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588  
R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812  
20 R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720  
R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388  
R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378  
25 R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382  
R-OVARC1000431//HS\_2199\_A2\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722  
R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662  
30 R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043  
R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381  
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583  
35 R-OVARC1000461//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417  
R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-81:489:91//AF023451  
R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526  
40 R-OVARC1000473//Homo sapiens full-length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851  
R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671  
R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984  
R-OVARC1000496  
45 R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005  
R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024  
R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510  
50 R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831  
R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069  
R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197  
55 R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//AC004223  
R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit

(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

5 R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC 1000605

10 R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162.

15 R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

20 R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130\_H\_16, complete sequence.//6.9e-48:525:73//AC005585

25 R-OVARC1000730//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

30 R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

35 R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

40 R-OVARC1000862//M.musculus FIF mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

45 R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS\_3082\_A2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

50 R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

55 R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS\_2195\_A2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

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R-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

5 R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

10 R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp).//2.2e-07:223:70//X91255

R-OVARC1000984

15 R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca<sup>2+</sup>/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//5.8e-71:332:87//AC003957

20 R-OVARC1001000//HS\_3032\_B1\_G11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190

25 R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813

R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345

30 R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//9.7e-17:180:78//AC005410

35 R-OVARC1001044

R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237

40 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657

R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276

R-OVARC1001074//HS\_2205\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

45 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272

50 R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270

R-OVARC1001161//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680

55 R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781

R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//

1.3e-28:427:70//AC004963  
R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859  
5 R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549  
R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213  
R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907  
10 R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796  
R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462  
R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794  
15 R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//1.4e-41:284:87//AC006071  
R-OVARC1001243//HS\_2055\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142  
R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148  
R-OVARC1001268  
20 R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551  
R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494  
R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062  
25 R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018  
R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142  
R-OVARC1001329//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402  
30 R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862  
R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242  
R-OVARC1001341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818  
35 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874  
R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350  
40 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297  
R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//0.20:335:60//AC005863  
R-OVARC 1001369  
R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210  
45 R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491  
R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//9.3e-20:422:60//AC005821  
R-OVARC1001391  
50 R-nnnnnnnnnnnn  
R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB00665  
R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668  
55 R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157  
R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341  
R-OVARC1001442  
R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086

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R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655

R-OVARC1001480//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676

5 R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507

R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039

10 R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488

R-OVARC1001547

15 R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165

R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418

R-OVARC1001610//HS\_3070\_A2\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523

20 R-OVARC1001611//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423

R-OVARC1001615//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658

R-OVARC1001668//HS\_3228\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379

25 R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965

R-OVARC1001703

R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194

30 R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145

R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276

R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257

35 R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575

R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279

40 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066

R-OVARC1001795

R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337

45 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694

R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585

50 R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046

R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086

55 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688

R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905

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R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350  
R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611  
R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
5 complete sequence.//9.1e-20:206:80//AL031864  
R-OVARC1001880//RPC111-42115.TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey se-  
quence.//3.9e-50:287:88//AQ052700  
R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//6.1e-13:457:63//  
AC003950  
10 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
2.5e-86:346:90//AF061749  
R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//  
7.2e-89:421:100//AF072246  
R-OVARC1001911//Homo sapiens full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315  
15 R-OVARC1001916  
R-OVARC1001928  
R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166  
R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region  
(env) gene, partial cds.//0.14:173:64//U58826  
20 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:  
63//M99593  
R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//8.2e-38:385:  
75//AC005666  
R-OVARC1001987  
25 R-OVARC1001989//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11,  
WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841  
R-OVARC1002044//Human DNA sequence from clone 6B1J21 on chromosome 1q23.2-24.3 Contains CpG island,  
complete sequence.//5.0e-42:298:86//AL031286  
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934  
30 R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//  
0.23:210:61//AC004411  
R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
5.4e-99:546:92//AC006015  
R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glypican-3  
35 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174  
R-OVARC1002127  
R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP Homo sapiens genomic clone 2290O18, genomic survey se-  
quence.//2.4e-07:316:62//AQ003988  
R-OVARC1002143//RPC111-54M8.TJ RPC111 Homo sapiens genomic clone R-54M8, genomic survey sequence.//  
40 2.3e-35:220:90//AQ083241  
R-OVARC1002156  
R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey se-  
quence.//1.6e-12:140:79//AQ265720  
R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey se-  
45 quence.//5.0e-59:291:99//AQ020420  
R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060  
R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981  
R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507  
50 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557  
R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING  
DRAFT SEQUENCE.//2.8e-44:405:77//D83253  
R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//  
AC006162  
55 R-PLACE1000040//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5,  
WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855  
R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462  
R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

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DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505  
 R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154  
 R-PLACE1000066  
 R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6  
 5 unordered pieces.//1.2e-87:456:95//AC005848  
 R-PLACE1000081  
 R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence.//  
 2.3e-83:409:98//AQ282619  
 R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746\_E\_8, complete sequence.//1.8e-06:420:57//  
 10 AC005358  
 R-PLACE1000142  
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//  
 AF058291  
 R-PLACE1000185  
 15 R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey se-  
 quence.//8.2e-80:410:97//AQ022149  
 R-PLACE1000214//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-09, complete  
 sequence.//1.6e-05:548:59//AL008989  
 R-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING  
 20 DRAFT SEQUENCE.//2.2e-16:118:91//AL032818  
 R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122  
 R-PLACE1000292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING  
 DRAFT SEQUENCE.//6.6e-41:322:84//Z98200  
 R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281\_F\_24, complete sequence.//1.8e-16:598:62//  
 25 AC004706  
 R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//  
 AC005326  
 R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:  
 492:58//AC005278  
 30 R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:  
 59//AE001364  
 R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//  
 AF073997  
 R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-  
 35 17:152:83//AC005015  
 R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//  
 0.51:346:58//AB020742  
 R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15,  
 WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009  
 40 R-PLACE1000421//HS\_2251\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807  
 R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//  
 AC002073  
 R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:  
 45 76//AF015724  
 R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.0e-54:429:  
 81//AC005899  
 R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector  
 pEMBLcos2, complete sequence.//0.66:103:72//AF059580  
 50 R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA  
 repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166  
 R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//  
 U35245  
 R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 55 DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308  
 R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//  
 AC004790  
 R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409



- R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302
- R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799\_N\_11, complete sequence.//1.5e-37:414:74//AC005323
- 5 R-nnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542
- R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506
- 10 R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059
- 15 R-PLACE1000610//HS\_3071\_A1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341
- R-PLACE1000636//HS\_3220\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157
- 20 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265
- R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896
- R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219
- 25 R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408
- R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300
- R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547
- R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791
- 30 R-PLACE1000755//HS\_2183\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202
- R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847
- 35 R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548
- R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970
- R-nnnnnnnnnnnn
- R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904
- 40 R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081
- R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334
- R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272
- 45 R-PLACE1000863
- R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505
- 50 R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489
- R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337
- R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//8.3e-20:223:76//AC005553
- 55 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506
- R-PLACE1000979
- R-PLACE1001000//CIT-HSP-2297I8.TF CIT-HSP Homo sapiens genomic clone 2297I8, genomic survey se-

quence.//7.0e-07:64:95//AQ004997  
 R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607  
 R-PLACE1001010  
 R-PLACE1001015//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING  
 5 DRAFT SEQUENCE.//1.5e-16:452:63//AL022318  
 R-PLACE1001024//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING  
 DRAFT SEQUENCE.//0.99:186:63//AL024498  
 R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-  
 15:313:68//AC005377  
 10 R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//  
 AC003664  
 R-PLACE1001076  
 R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on  
 chromosome X contains ESTs.//0.97:332:59//Z74696  
 15 R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07 :302:62//AC005139  
 R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:  
 60//AE001372  
 R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5')  
 20 two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and  
 STSs, complete sequence.//4.9e-06:334:60//Z84480  
 R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2  
 ordered pieces.//1.1e-31:331:75//AC005412  
 R-PLACE1001168//HS\_2036\_A1\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662  
 R-PLACE1001171  
 R-PLACE1001185  
 R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139  
 R-PLACE1001241//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete  
 30 sequence.//0.11:258:61//AL008972  
 R-PLACE1001257//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B4P3; HTGS  
 phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016  
 R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//  
 AF045448  
 35 R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839  
 R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey se-  
 quence.//5.4e-24:147:76//AQ042129  
 R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642  
 R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and  
 40 R32804, complete sequence.//2.2e-22:139:77//AC003682  
 R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286  
 R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5')  
 two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and  
 STSs, complete sequence.//7.2e-39:308:83//Z84480  
 45 R-PLACE1001351//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y39B6,  
 WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399  
 R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//  
 D89927  
 R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615  
 50 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030  
 R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319  
 R-PLACE1001387  
 R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355  
 R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2  
 55 ordered pieces.//6.7e-70:352:98//AC005412  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087  
 R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.12:53:84//  
 AC006241

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R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111

5 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130

R-PLACE1001468//HS\_3050\_A2\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920

R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368

10 R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401

R-PLACE1001503//HS\_2183\_A1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613

R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969

15 R-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667

R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_L\_16, complete sequence.//2.6e-18:171:82//AC 005669

R-PLACE1001551

20 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135

R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860

R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605

R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037

25 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174

R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878

R-PLACE1001634//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791

30 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//2.6e-83:441:95//AC005971

R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253

R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250

35 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077

R-PLACE1001705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716

R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349

40 R-PLACE1001720

R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120

R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261

45 R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027

R-PLACE1001745

R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509

50 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243

R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463

R-PLACE1001761

R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426

R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711

55 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//

4.1e-92:463:95//AF058953  
 R-PLACE1001821//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567  
 R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351  
 5 R-PLACE1001869  
 R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011  
 R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567  
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671  
 10 R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//0.98:248:60//AC005245  
 R-PLACE1001983//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389  
 R-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
 15 DRAFT SEQUENCE.//1.4e-44:376:80//AL023755  
 R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117  
 R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900  
 20 R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438  
 R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763  
 R-PLACE1002073  
 R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302  
 25 R-PLACE1002115//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344  
 R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527  
 R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.  
 30 Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706  
 R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849  
 35 R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785  
 R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456  
 40 R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056  
 R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152  
 45 R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071  
 R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907  
 50 R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255  
 R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505  
 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271  
 R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329  
 55 R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939  
 R-PLACE1002433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

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R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542  
R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey  
sequence.//0.70:247:61//AQ242104  
5 R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3//  
0.00060:471:59//AJ229041  
R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
2.5e-10:98:81//AC004854  
R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262  
10 R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545  
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-  
53:307:91//AF042273  
15 R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551  
R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey se-  
quence.//3.2e-42:297:85//AQ037614  
R-PLACE1002514//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
DRAFT SEQUENCE.//7.8e-16:221:73//Z95114  
20 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256  
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//  
AC004774  
R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//  
0.0042:489:60//D16253  
25 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178  
R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:  
292:84//AC006084  
R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete  
cds.//3.1e-17:517:61//AF045555  
30 R-PLACE1002591  
R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626  
R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:  
65//U63313  
R-PLACE1002625//HS\_2233\_B2\_H04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663  
35 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//  
AF079765  
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-  
77:390:97//AF068180  
40 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656  
R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723  
R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library)  
complete sequence.//0.0098:197:64//AC005185  
R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:  
82//AC006145  
45 R-PLACE1002782  
R-PLACE1002794  
R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey se-  
quence.//6.0e-50:250:100//AQ034981  
R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279  
50 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC li-  
brary) complete sequence.//6.3e-59:339:93//AC004466  
R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//  
M27877  
55 R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74//  
AC004819  
R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey se-  
quence.//0.0011:210:61//AQ040519  
R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

R-PLACE1002881  
R-PLACE1002908//HS\_3064\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985  
R-PLACE1002941  
5 R-PLACE1002962  
R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARΔ for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs,  
10 STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721  
R-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755  
R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921  
15 R-PLACE1002996//HS\_2064\_A1\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211  
R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145  
R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.3e-95:465:98//  
20 AC005920  
R-PLACE1003044  
R-PLACE1003092//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266  
R-PLACE1003100//HS\_2244\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence.//2.3e-42:288:86//AQ084224  
25 R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885  
R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558  
R-PLACE1003145  
30 R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616  
R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479  
R-PLACE1003176  
35 R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095  
R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551  
R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139  
40 R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11.//7.6e-114:567:96//AF086432  
R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416  
R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099  
R-PLACE1003258  
45 R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952  
R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9.//1.7e-91:458:96//M27877  
R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete  
50 sequence.//4.3e-34:370:71//Z82243  
R-PLACE1003342//CIT-HSP-2311D21.TF.CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460  
R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153  
55 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715  
R-PLACE1003361

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R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805  
R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174  
5 R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//1.2e-62:434:83//AC004771  
R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350  
R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878  
10 R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//2.4e-13:175:76//AC005695  
R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587  
R-PLACE1003454//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//0.47:411:58//AL009014  
15 R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125  
R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.6e-37:319:81//AC006080  
R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480  
20 R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859  
R-PLACE1003521//HS\_3252\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562  
25 R-PLACE1003528//HS\_2041\_B1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483  
R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404  
30 R-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297  
R-PLACE1003566  
R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965  
35 R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571  
R-PLACE1003584  
R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032  
R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066  
R-PLACE1003596//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597  
40 R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200  
R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081  
R-nnnnnnnnnnnnn  
45 R-PLACE1003618//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451  
R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688  
R-PLACE1003638//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312  
50 R-PLACE1003669//HS\_3054\_A2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713  
R-PLACE1003704//HS\_3213\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784  
55 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067  
R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607  
R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-

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44:505:73//AL022336  
R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357  
R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023  
5 R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//  
AC003070  
R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//5.4e-12:189:  
71//AC005919  
R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//  
AC004160  
10 R-PLACE1003783  
R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:  
204:74//AC004659  
R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey se-  
quence.//7.0e-37:234:89//AQ114933  
15 R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558  
R-PLACE1003850  
R-PLACE1003858  
R-nnnnnnnnnnnnn  
R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete se-  
20 quence.//8.7e-33:285:81//AC000072  
R-nnnnnnnnnnnnn  
R-PLACE1003886  
R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//  
AC004069  
25 R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810  
R-PLACE1003903//Homo sapiens full-length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422  
R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete  
cds.//0.56:247:61//U73520  
R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281  
30 R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:  
342:85//Z74022  
R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030  
R-PLACE1003968//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-62, complete  
sequence.//1.3e-07:245:65//AL010247  
35 R-PLACE1004104  
R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485  
R-PLACE1004118//HS\_3092\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3092 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151  
R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-  
40 06:193:66//AF022085  
R-PLACE1004149//HS\_2253\_A2\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711  
R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC  
Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295  
45 R-PLACE1004161  
R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071  
R-PLACE1004197//RPC111-69N15.TK RPC111 Homo sapiens genomic clone R-69N15, genomic survey se-  
quence.//0.0078:170:65//AQ265515  
R-PLACE1004203//Homo sapiens semaphorin L (SEMA) mRNA, complete cds.//3.4e-105:501:98//AF030698  
50 R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic  
marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//  
AL021326  
R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:  
61//AC006031  
55 R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete  
sequence.//3.4e-09:576:59//AC004470  
R-PLACE1004258//HS\_3034\_A1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936



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R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234

5 R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308

R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//5.8e-31:340:75//AC005920

10 R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095

R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588

R-PLACE1004336//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383

15 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817

20 R-PLACE1004388//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027

25 R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532

R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296

R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283

30 R-PLACE1004451//HS\_2258\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189

R-PLACE1004460

R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621

35 R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333:70//AC004389

R-PLACE1004473

R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584

40 R-PLACE1004506

R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427

R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071

45 R-PLACE1004518

R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666

R-PLACE1004550

50 R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931

R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800

R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136

55 R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876

R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343

R-nnnnnnnnnnnn//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey se-

quence.//2.2e-81:433:94//AQ283692  
 R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561  
 R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606  
 5 R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860  
 R-PLACE1004686  
 R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859  
 10 R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448  
 R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965  
 R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507  
 15 R-PLACE1004736  
 R-PLACE1004740  
 R-nnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556  
 20 R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//AC002523  
 R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367  
 R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010  
 25 R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269  
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178  
 R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140  
 30 R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250  
 R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126  
 R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666  
 35 R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human-BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669  
 R-PLACE1004836//HS\_2270\_A2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110  
 40 R-PLACE1004838//CIT-HSP-2343E10.TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544  
 R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820  
 R-PLACE1004868//Human Chromosome X clone bWDX342, complete sequence.//0.57:344:59//AC004072  
 R-PLACE1004885//HS\_3235\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193  
 45 R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577  
 50 R-PLACE1004902  
 R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209  
 R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605  
 55 R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936  
 R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683  
 R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788

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R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494

R-PLACE1004972

R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970

5 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308

R-PLACE1004985//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522

10 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925

R-PLACE1005027

R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775

15 R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867

R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584

20 R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556

R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//2.1e-42:384:69//AC005495

R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788

25 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401

R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476

R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195

R-PLACE1005111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845

30 R-PLACE1005128

R-PLACE1005146

R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140

35 R-PLACE1005181//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018

R-PLACE1005181//HS\_2182\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787

R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161

40 R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043

R-PLACE1005232//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476

R-PLACE1005243

R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132

45 R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067

R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720

R-PLACE1005287//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744

50 R-PLACE1005305//HS\_3180\_B2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443

R-PLACE1005308

R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383

55 R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960

R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794

R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380

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R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195  
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//3.0e-44:434:77//  
AC005291  
5 R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991  
R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//  
AC002477  
R-PLACE1005467//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE.//1.1e-40:328:81//Z93014  
10 R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-  
notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310  
R-PLACE1005477//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING  
DRAFT SEQUENCE.//0.020:216:66//AL023693  
15 R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//  
2.8e-44:327:70//AC005392  
R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164\_O\_3, complete sequence.//4.2e-23:284:  
74//AC004703  
20 R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631  
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185  
R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468  
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SE-  
QUENCE.//2.3e-76:395:96//AP000038  
25 R-PLACE1005530//C.familiaris CA repeat sequence (isolate ).//0.023:90:75//X86184  
R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:  
64//AL025928  
R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.069:305:60//  
AC005969  
30 R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//4.3e-105:587:  
91//AC004707  
R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971  
R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:  
77//AC004991  
35 R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//  
AC004126  
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//  
U72788  
R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599  
40 R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405  
R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
ordered pieces.//5.6e-79:270:94//AC005840  
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382  
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//  
AF083255  
45 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//8.6e-08:505:  
58//AC005701  
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and  
polymorphic CA repeat.//3.2e-27:307:72//Z82203  
50 R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey se-  
quence.//0.030:91:70//B15144  
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II  
(COL2A1) gene.//5.2e-10:587:59//L10171  
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810  
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635  
55 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601  
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//D42087  
R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024  
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//

AC004827  
 R-PLACE1005803  
 R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75//  
 AC002530  
 5 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1  
 ordered pieces.//2.9e-56:333:91//AC004150  
 R-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING  
 DRAFT SEQUENCE.//0.020:513:55//AL031745  
 R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763 R-PLACE1005850  
 10 R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-  
 06:318:63//AC004887  
 R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931  
 R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chro-  
 mosome X contains STS.//1.0e-06:306:64//Z70281  
 15 R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139  
 R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21,-genomic survey se-  
 quence.//4.8e-84:494:89//AQ261347  
 R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//  
 20 8.3e-97:520:93//AQ237243  
 R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS,  
 complete sequence.//5.2e-67:578:78//AL022719  
 R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654  
 R-PLACE1005934  
 25 R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//  
 0.00021:272:62//AF069716  
 R-PLACE1005951  
 R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429  
 R-PLACE1005955//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131  
 30 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, com-  
 plete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial  
 RNAs.//7.0e-09:549:59//AF044863  
 R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086  
 R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE,  
 35 51 ordered pieces.//4.4e-63:369:91//AC005866  
 R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177  
 R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375  
 R-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog PARP mRNA, complete cds.//1.1e-32:  
 266:83//AF072521  
 40 R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete se-  
 quence.//1.8e-17:164:82//AC000077  
 R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139  
 R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906  
 R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-  
 45 18:220:74//AC004885  
 R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63//  
 AJ005122  
 R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete  
 sequence.//0.43:178:65//AC005454  
 50 R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68//  
 AC004849  
 R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455:59//Z98551  
 R-PLACE1006157//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//0.00018:351:60//AL034557  
 55 R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01\_124\_D\_3 map 10q25.1, WORKING DRAFT  
 SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006103  
 R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-  
 chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-

28:342:75//U91328  
 R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555  
 R-nnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972  
 R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433  
 5 R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//  
 AC004410  
 R-PLACE1006196  
 R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398  
 R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on  
 10 chromosome X contains ESTs.//0.041:215:61//Z73362  
 R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877  
 R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970  
 R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//  
 AC004142  
 15 R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
 0.029:499:56//AC006034  
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548  
 R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
 quence.//0.00043:160:66//AC004087  
 20 R-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING  
 DRAFT SEQUENCE.//3.5e-120:611:96//AL031320  
 R-PLACE1006318  
 R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560  
 R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987  
 25 R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276  
 R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:  
 56//AE001398  
 R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630  
 R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:  
 30 574:91//AC004232  
 R-PLACE1006382  
 R-PLACE1006385//Mus musculus intersectin-EH binding protein lbp2 mRNA, partial cds.//1.4e-50:350:86//  
 AF057286  
 R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
 35 5.1e-51:339:82//AC004854  
 R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//1.6e-38:297:84//AC004804  
 R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985  
 R-PLACE1006445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING  
 40 DRAFT SEQUENCE.//3.0e-07:376:61//AL031726  
 R-PLACE1006469  
 R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152  
 R-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING  
 DRAFT SEQUENCE.//3.0e-101:535:94//AL021977  
 45 R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//0.78:44:95//  
 AC005972  
 R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100  
 R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey se-  
 quence.//9.0e-17:414:61//B75158  
 50 R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197  
 R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934  
 R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//  
 AC004209  
 R-PLACE1006552//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
 55 WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865  
 R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
 DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//

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2.9e-116:590:95//U97670  
R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050  
R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331  
5 R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128  
R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038  
R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882  
10 R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024  
R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154  
15 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172  
R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626  
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622  
R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984  
20 R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865  
R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599  
25 R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083  
R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793  
R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507  
30 R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174  
R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062  
35 R-PLACE1006829  
R-PLACE1006860  
R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378  
40 R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155  
R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232  
R-nnnnnnnnnnnnn  
45 R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203  
R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184  
R-PLACE1006932  
R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061  
50 R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482  
R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//6.7e-42:295:86//AC005544  
R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349  
55 R-PLACE1006966//HS\_2219\_B2\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequencer.//0.019:180:63//AQ145873  
R-PLACE1006989  
R-PLACE1007014

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R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845

R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693

5 R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895

R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368

10 R-PLACE1007105//Mus musculus muskulin mRNA, complete cds.//2.7e-32:379:73//U72194

R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688

15 R-PLACE1007112//Cynops cornifex cytb gene.//0.020:427:58//AJ228479

R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09.//5.7e-107:535:96//AF074987

R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050

R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283

20 R-PLACE1007226

R-PLACE1007238

R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495

R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454

25 R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970

R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908

R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.4e-10:135:74//AC006080

30 R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291

R-PLACE1007282//B.garinii (strain Tls1) p83/100 gene (partial).//0.95:183:60//X81533

R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158

35 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195

R-PLACE1007317//Drosophila dasyncemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253

40 R-PLACE1007342

R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870

R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507

45 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709

R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261

R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

50 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

55 R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081

R-PLACE1007460

R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-



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brary) complete sequence.//7.0e-08:335:60//AC004241  
R-PLACE1007484  
R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373  
5 R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559  
R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-79:387:96//AC004231  
R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682  
10 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381  
R-PLACE1007544  
R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds.//4.0e-17:108:97//U77706  
R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465  
15 R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665  
R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179  
R-PLACE1007618  
R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176  
20 R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840  
R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408  
R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149  
25 R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367  
R-PLACE1007688  
R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044  
30 R-PLACE1007697  
R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662  
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243  
R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854  
35 R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//3.8e-53:415:81//U60269  
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585  
R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169  
R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560  
40 R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820  
R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z37981  
R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116  
45 R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104  
R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//0.00052:455:61//AC002379  
R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275  
R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15,  
50 WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010  
R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021  
R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309  
R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete  
55 sequence.//1.6e-43:551:70//AL022162  
R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754

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R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956

5 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095

R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157

10 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529

R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262

15 R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933

R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346

R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628

20 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840

R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592

25 R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232

R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036

R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157

30 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919

R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955

R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939

35 R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849

R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

R-PLACE1008198

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102

40 R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549

R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688

R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562

45 R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-nnnnnnnnnnnnn

R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272

R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308

50 R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886

R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176

R-PLACE100833//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226

55 R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR.//2.5e-98:556:90//AF036145

R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

- R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011
- R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244
- 5 R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417
- R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604
- R-nnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326
- 10 R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177
- R-PLACE1008424
- R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864
- 15 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576
- R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335
- R-PLACE1008455
- 20 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526
- R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696
- R-PLACE1008488
- 25 R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778
- R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555
- R-PLACE1008532
- 30 R-PLACE1008533
- R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623
- R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074
- 35 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120
- R-nnnnnnnnnnnnn
- R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297
- R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836
- 40 R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826
- R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096
- R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001
- 45 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333
- R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742
- R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406
- 50 R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147
- R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841
- 55 R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864
- R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

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R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088  
R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AQ079210  
5 R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933  
R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581  
10 R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058  
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932  
15 R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G\_17, complete sequence.//0.0022:409:60//AC005820  
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
20 R-PLACE1008934  
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//9.8e-84:429:92//AC005495  
R-PLACE1008947  
R-PLACE1009020  
25 R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
30 R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//2.9e-06:160:70//AC004707  
R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694  
35 R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074  
R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783  
40 R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
R-PLACE1009099  
R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025  
45 R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551  
R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929  
50 R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031  
R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876  
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//2.8e-44:360:71//AC005972  
55 R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925  
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and

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STSS, complete sequence.//1.9e-46:572:69//Z84480  
R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070  
R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560  
R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248  
5 R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392  
R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818  
R-PLACE1009308  
10 R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801  
R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:85//AC006120  
R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176  
15 R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140  
R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989  
R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915  
20 R-PLACE1009388  
R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61//AC002427  
R-nnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038  
25 R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:96//AC005919  
R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598  
30 R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151  
R-PLACE1009459  
R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531  
35 R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213  
R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321  
R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160  
40 R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427  
45 R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614  
R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146  
R-PLACE1009581  
50 R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006  
R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051  
R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230  
55 R-PLACE1009613//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266  
R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222  
R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

- sequence.//0.72:176:62//B81271  
 R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276  
 R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811
- 5 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159  
 R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075  
 R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534  
 R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011  
 R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109
- 10 R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398  
 R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024  
 R-PLACE1009794
- 15 R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996  
 R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172  
 R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672
- 25 R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945  
 R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116  
 R-nnnnnnnnnnnn
- 30 R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005  
 R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412  
 R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673
- 35 R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308  
 R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483
- 40 R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247  
 R-PLACE1009992  
 R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367
- 45 R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874  
 R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513  
 R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775
- 50 R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692  
 R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094
- 55 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482  
 R-PLACE1010076//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699  
 R-PLACE1010083

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R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59/B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

5 R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

10 R-PLACE1010134

R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

15 R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

20 R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

25 R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cpg85a61rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

30 R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

35 R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675

40 R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

45 R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

50 R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein varl.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370

55 R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

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R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

5 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467

10 R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

15 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

20 R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682

25 R-PLACE1010802//Phoebis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524

30 R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507:90//AB020868

35 R-PLACE1010870//RPCI11-59K21:TK RPCI11 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

40 R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

45 R-PLACE1010917

R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-PLACE1010944//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243

50 R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

55 R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522

R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//



AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

5 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

10 R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

15 R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006

20 R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968

25 R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

30 R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

35 R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

40 R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

45 R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

50 R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

55 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//0.99:267:60//

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AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

5 R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

10 R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

15 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

20 R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

25 R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

30 R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

35 R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478

40 R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

45 R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

50 R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

55 R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence//3.0e-55:299:86//  
 5 AC006236  
 R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey se-  
 quence//4.5e-54:295:94//AQ058140  
 R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)//6.5e-38:298:82//X69907  
 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces//5.3e-  
 10 34:200:79//AC005628  
 R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence//1.8e-49:274:89//  
 AC003083  
 R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey se-  
 quence//1.8e-48:389:79//AQ112243  
 15 R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING  
 DRAFT SEQUENCE//0.0027:95:76//AL022315  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.9e-39:429:72//AB011147  
 R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces//  
 5.9e-40:310:84//AC004832  
 20 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds//1.9e-109:550:95//AF027219  
 R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces//1.6e-106:553:95//AC005910  
 R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part  
 of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence//1.8e-  
 25 38:285:84//AL031730  
 R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING  
 DRAFT SEQUENCE//4.3e-113:559:97//AL031848  
 R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1//0.00041:347:61//  
 X16325  
 30 R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite//0.50:165:63//U63067  
 R-PLACE2000132  
 R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete  
 sequence//0.0032:310:61//AL008974  
 R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING  
 35 DRAFT SEQUENCE//1.1e-111:566:96//AL020995  
 R-PLACE2000164  
 R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.9e-40:390:76//AC005598  
 R-PLACE2000172  
 40 R-PLACE2000176  
 R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
 DRAFT SEQUENCE//8.7e-45:298:87//AL008718  
 R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end//5.6e-88:495:92//L02897  
 R-PLACE2000223  
 45 R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3159 Col=11 Row=D, genomic survey sequence//1.8e-88:454:96//AQ179271  
 R-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58  
 unordered pieces//9.1e-41:282:86//AC005902  
 R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence//8.3e-35:305:80//Z97181  
 50 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence//3.5e-18:325:  
 67//AC002394  
 R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence//1.5e-39:287:85//  
 AC003043  
 55 R-PLACE2000305//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING  
 DRAFT SEQUENCE//1.2e-43:295:85//Z93015  
 R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-  
 threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

- TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542  
 R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147
- 5 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880  
 R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147  
 R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963
- 10 R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291  
 R-PLACE2000371  
 R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734
- 15 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917  
 R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432  
 R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059
- 20 R-PLACE2000399  
 R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216  
 R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273  
 R-PLACE2000419
- 25 R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528  
 R-PLACE2000427  
 R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379  
 R-PLACE2000435
- 30 R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521  
 R-PLACE2000450 4.1e-42:328:79//AG006257  
 R-PLACE2000455  
 R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence.//5.1e-116:570:97//AC005740
- 35 R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460  
 R-PLACE2000477//M.musculus tex264 mRNA (3'region).//7.5e-06:117:76//X80427  
 R-PLACE3000004  
 R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976
- 40 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267  
 R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648  
 R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156
- 45 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026  
 R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200  
 R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645
- 50 R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023  
 R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735  
 R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237
- 55 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//6.9e-106:549:94//AC005277  
 R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

R-PLACE3000157  
 R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500  
 R-PLACE3000160  
 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//  
 5 AC006130  
 R-PLACE3000194  
 R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//7.2e-61:394:89//  
 AC005291  
 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for  
 10 neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD)1 N-  
 acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1  
 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.23:309:57//U52112 R-  
 PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
 quence.//1.1e-15:156:81//B54637  
 15 R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING  
 DRAFT SEQUENCE.//1.3e-16:139:87//AL031594  
 R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720  
 R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363:80//  
 20 AC004167  
 R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786  
 R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and  
 lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626  
 R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I35489  
 25 R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169  
 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307  
 R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 DRAFT SEQUENCE.//3.9e-54:492:77//AL034379  
 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//  
 30 AC004081  
 R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//  
 AC005328  
 R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING  
 DRAFT SEQUENCE.//6.2e-51:314:84//Z98884  
 35 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-  
 44:289:90//U93037  
 R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006  
 R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.1e-43:230:84//AC005480  
 40 R-PLACE3000339  
 R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence.//2.5e-111:550:97//AC006055  
 R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and  
 GSSs, complete sequence.//1.5e-44:314:78//AL022323  
 45 R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142  
 R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5,  
 WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712  
 R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197  
 50 R-PLACE3000363  
 R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487:76//AC002465  
 R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699  
 R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING  
 55 DRAFT SEQUENCE.//6.4e-61:515:81//AL008722  
 R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 0.00098:444:60//AC005231  
 R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

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DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506  
R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
8.0e-47:223:81//AC006023  
5 R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003  
R-PLACE3000405//Homo sapiens chromosome 7q telo BAC F6, complete sequence.//2.4e-44:466:74//AF104455  
R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
DRAFT SEQUENCE.//7.7e-49:471:75//AL008718  
R-PLACE3000413  
10 R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SE-  
QUENCE.//5.4e-42:416:77//AJ009612  
R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal  
protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627  
R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING  
DRAFT SEQUENCE.//3.8e-98:549:92//AL031284  
15 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//  
U43899  
R-PLACE3000477  
R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heyman nephritis antigen  
gp330.//6.6e-17:344:68//Z11995  
20 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352  
R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984  
R-PLACE4000049//Human BAC clone GS165104 from 7q21, complete sequence.//0.29:313:59//AC002379  
25 R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE.//0.0058:466:57//AL034557  
R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356  
R-PLACE4000089//RPCI11-15I1.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-15I1, genomic survey se-  
quence.//3.2e-07:284:60//B82414  
30 R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506  
R-PLACE4000100  
R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010  
R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:  
90//AC003007  
35 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//  
AB007969  
R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//  
AC005034  
R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a  
40 pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde  
dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939  
R-PLACE4000192  
R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
5.4e-44:280:82//AC005631  
45 R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981  
R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//5.7e-59:558:  
76//AC005821  
R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey se-  
quence.//1.7e-44:313:84//AQ037381  
50 R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.5e-39:311:83//  
AC005920  
R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:  
61//Z80410  
R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:  
55 68//AC005510  
R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675  
R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339  
R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

sequence.//8.2e-41:295:85//Z99495  
 R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640  
 R-PLACE4000326  
 R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//  
 5 AC005587  
 R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829  
 R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222  
 R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING  
 10 DRAFT SEQUENCE.//1.7e-05:160:65//AL022312  
 R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-  
 47:351:81//AC004913  
 R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown  
 gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377  
 15 R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT  
 SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406  
 R-PLACE4000411  
 R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
 0.028:91:78//AC005628  
 20 R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING  
 DRAFT SEQUENCE.//1.6e-43:532:71//AL022156  
 R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:  
 357:61//AE001427  
 R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC  
 25 Library) complete sequence.//2.7e-37:416:74//AC005865  
 R-PLACE4000522  
 R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//0.0020:383:60//AC005342  
 R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC li-  
 30 brary) complete sequence.//2.9e-44:465:75//AC002996  
 R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING  
 DRAFT SEQUENCE.//2.2e-43:354:82//Z83844  
 R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:  
 327:60//AE001422  
 35 R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318  
 R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157  
 R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573  
 40 R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567  
 R-THYRO1000085  
 R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//3.3e-36:301:78//AF104455  
 R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING  
 DRAFT SEQUENCE.//1.4e-35:282:82//AL033528  
 45 R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-  
 32:351:65//AC002300  
 R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:  
 85//U91318  
 R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
 50 ordered pieces.//0.66:334:59//AC005840  
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142  
 R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
 DRAFT SEQUENCE.//1.1e-40:298:84//Z95114  
 R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//3.4e-37:425:  
 55 73//AC005703  
 R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey  
 sequence.//8.4e-38:276:84//B63536  
 R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

70:553:81//Z83841  
 R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING  
 DRAFT SEQUENCE.//6.7e-41:345:81//AL031732  
 R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial  
 cds for thymopoietin beta.//1.3e-43:356:80//U18271  
 R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//  
 AC004139  
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698  
 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552  
 R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482  
 R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 con-  
 taining COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115  
 R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//  
 4.8e-58:447:81//AC000039  
 R-THYRO 1000242  
 R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains  
 the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein  
 CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete se-  
 quence.//3.4e-56:300:84//Z95152  
 R-THYRO1000270  
 R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING  
 DRAFT SEQUENCE.//4.8e-113:584:96//AL031664  
 R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068  
 R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366  
 R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058  
 R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333  
 R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091  
 R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777  
 R-nnnnnnnnnnnnn  
 R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:  
 93//AC006019  
 R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
 WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078  
 R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523  
 R-THYRO 1000401  
 3.3e-111:546:97//AF051907  
 R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 2.7e-44:289:89//AC005231  
 R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//6.7e-27:222:  
 82//AC005668  
 R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING  
 DRAFT SEQUENCE.//2.4e-36:369:76//AL021391  
 R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962  
 R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-  
 95:512:94//AC005740  
 R-THYRO1000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586  
 R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987  
 R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//  
 AC004798  
 R-THYRO1000558  
 R-THYRO 1000569  
 R-THYRO1000570//Homo sapiens full-length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408  
 R-nmmmmnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587  
 R-THYRO 000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear  
 gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072



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R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675  
R-THYRO 1000605  
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//  
AC005546  
5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs  
and GSSs, complete sequence.//4.0e-06:249:63//AL022323  
R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998  
R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572  
R-nnnnnnnnnnnnn  
10 R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains  
endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005  
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:  
64//AC004069  
R-THYRO1000684  
15 R-THYRO1000699  
R-THYRO1000712  
R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460  
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660  
20 R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558  
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey se-  
quence.//1.2e-81:391:99//AQ038226  
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//  
AC004617  
25 R-THYRO1000793  
R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered piec-  
es.//4.7e-40:362:76//AC002555  
30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788  
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angel-  
man Syndrome region, complete sequence.//3.3e-57:522:76//AC004738  
35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE,  
9 unordered pieces.//4.2e-17:291:69//AC005849  
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs,  
complete sequence.//1.1e-41:419:75//AL031592  
R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-  
40 ING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING  
DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
1.0e-97:554:92//AC006015  
45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:  
566:94//AF079529  
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ571I4, WORKING DRAFT SEQUENCE, 29 un-  
ordered pieces.//8.9e-61:479:81//AC004229  
50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//  
AF047440  
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//  
AC006126  
55 R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//0.99:71:78//  
AC005562  
R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727

5 R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677

10 R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070

R-THYRO1001120

15 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 2381I10, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

20 R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.r11a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145

R-THYRO1001177

25 R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO 1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

30 R-THYRO 1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

35 R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-nnnnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

40 R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

45 R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPCI11-69F22.TK RPCI1 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

50 R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

55 R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

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R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece.//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

5 R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876

10 R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

15 R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

20 R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

25 R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

30 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

35 R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnn

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

40 R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYRO1001793

45 R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

50 R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

55 R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-

56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5//0.64:203:63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cytosine zoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA10003131//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171:65//B88000

R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.diploperemnis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

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R-nnnnnnnnnnnnn/CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

5 R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

10 R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

15 R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

20 R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

25 R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259

R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

30 R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

35 R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112

40 R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

45 R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

50 R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221

55 R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,

complete sequence.//1.3e-35:207:95//AL034430  
R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336  
5 R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574  
R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151  
R-Y79AA1001555  
R-Y79AA1001585  
10 R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722  
R-Y79AA1001603//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766  
R-Y79AA1001613  
15 R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975  
R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008  
R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743  
20 R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792  
R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178  
R-Y79AA1001705  
R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139  
25 R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402  
R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044  
R-Y79AA1001827//Oryctolagus cuniculus PIUS mRNA, complete cds.//2.3e-90:557:89//U74297  
30 R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152  
R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369  
35 R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874  
R-Y79AA1001874  
R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650  
R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577  
40 R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465  
R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319  
45 R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011  
R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612  
R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence.//1.9e-44:245:96//AQ044502  
50 R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752  
R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey sequence.//8.5e-21:147:91//B75354  
R-Y79AA1002139  
55 R-Y79AA1002204  
R-nnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:59//U13616  
R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415  
R-Y79AA1002210

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R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133  
R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
DRAFT SEQUENCE.//5.9e-07:535:57//AL034557  
R-Y79AA1002229  
5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592  
R-Y79AA1002246  
R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384  
R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331  
10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534  
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//  
1.1e-07:368:61//AC005887  
R-Y79AA1002351  
R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a.//  
15 0.57:59:79//Z62206  
R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//2.0e-98:385:99//  
AC005920  
R-Y79AA1002407//Homo sapiens chromosome-17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:  
76//AC004662  
20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
quence.//6.3e-08:103:80//AC004087  
R-Y79AA1002431  
R-nnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284  
R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-  
25 103:525:96//AC006116  
R-Y79AA1002482//Homo sapiens chromosome. 18, clone hRPK.474\_N\_24, complete sequence.//9.7e-38:302:  
83//AC006238  
R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

### 30 Homology Search Result Data 4.

**[0307]** The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

**[0308]** Data include

35 the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

40 **[0309]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069  
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
L40157  
45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668  
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
myces cerevisiae]//0.00019:192:65//Hs.7900:W22411  
50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
342:61//Hs.14207:U86453  
55 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:  
AB018340  
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200  
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

Hs.135552:AI215187  
 F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309  
 F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079  
 5 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729  
 F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802  
 F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133  
 F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847  
 10 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529  
 F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984  
 F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289  
 F-HEMBA1000231  
 15 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377  
 F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703  
 F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460  
 F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562  
 F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568  
 20 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186  
 F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406  
 F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664  
 F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095  
 F-HEMBA1000303  
 25 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946  
 F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898  
 F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965  
 F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961  
 F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712  
 30 F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503  
 F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548  
 F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802  
 F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087  
 35 F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010  
 F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853  
 F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878  
 F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320  
 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520  
 40 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533  
 F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008  
 F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915  
 F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253  
 F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875  
 45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970  
 F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034  
 F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398  
 F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893  
 50 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875  
 F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590  
 F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853  
 F-HEMBA1000469  
 F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561  
 55 F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551  
 F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970  
 F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750



F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:  
 D13666  
 F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093  
 F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646  
 5 F-HEMBA1000518  
 F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881  
 F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:  
 84//Hs.155871:AA533783  
 F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:  
 10 87//Hs.22383:R51067  
 F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:  
 AA455706  
 F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080  
 F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809  
 15 F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389  
 F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:  
 K00629  
 F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684  
 F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729  
 20 F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:  
 AB018303  
 F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977  
 F-HEMBA1000568//EST//0.12:270:61//Hs.134833 :AI091046  
 F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042  
 25 F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681  
 F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//  
 Hs.55084:AA479162  
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:  
 AJ007509  
 30 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241  
 F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.0e-68:574:  
 79//Hs.159176:U92019  
 F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535  
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925  
 35 F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333  
 F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:  
 AA643235  
 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:  
 AB014590  
 40 F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174  
 F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582  
 F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912  
 F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073  
 F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878  
 45 F-HEMBA1000686  
 F-HEMBA1000702  
 F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309  
 F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850  
 F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630  
 50 F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881  
 F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491  
 F-HEMBA1000747  
 F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568  
 F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716  
 55 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239  
 F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803  
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216  
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

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F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843  
 5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237  
 10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154  
 F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
 15 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
 nomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046  
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537  
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142  
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:  
 20 AB011119  
 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//  
 Hs.111445:H00596  
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:  
 AA609476  
 25 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phos-  
 phoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199  
 F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//  
 0.080:128:71//Hs.118972:AA761369  
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161  
 30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903  
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775  
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314  
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.  
 159564:AF061936  
 35 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.  
 127338:AB007961  
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895  
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835  
 40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.  
 46468:U45984  
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:  
 AB007937  
 45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572  
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.  
 159897:AB007970  
 50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142  
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515  
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881  
 F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971  
 F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:  
 55 U06088  
 F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813  
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420  
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

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Hs.147802:R71297  
F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172  
F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248  
5 F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284  
F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017  
F-HEMBA1001099  
F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750  
F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497  
10 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940  
F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917  
F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747  
F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341  
15 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582  
F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457  
F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226  
F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499  
20 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463  
P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717  
F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694  
F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748  
25 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058  
F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046  
F-HEMBA1001265  
F-HEMBA1001281  
F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155  
30 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131  
F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741  
F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219  
F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590  
35 F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201  
F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873  
F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301  
F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861  
40 F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427  
F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013  
F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569  
45 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358  
F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794  
F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074  
F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156  
50 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353  
F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848  
F-HEMBA1001388  
F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660  
55 F-HEMBA1001398  
F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117  
F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017798  
F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

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F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726  
 5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:  
 80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:  
 AA573499  
 10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.  
 7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390  
 15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:  
 AB011144  
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451  
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219  
 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054  
 20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:  
 M19503  
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902  
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869  
 F-HEMBA1001526  
 25 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476  
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580  
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652  
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//  
 Hs.91589:M36205  
 30 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814  
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:  
 AJ012449  
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184  
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228  
 35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988  
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918  
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210  
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400  
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870  
 40 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//  
 0.038:198:64//Hs.34579:AI338536  
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899  
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204  
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560  
 45 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283  
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121  
 F-HEMBA1001661  
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:  
 669:99//Hs.107254:AC005943  
 50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.  
 158095:AB007953  
 F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788  
 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060  
 F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760  
 55 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995  
 F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836  
 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114  
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

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vegicus//3.0e-30:195:92//Hs.132948:AA194452  
F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554  
F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197  
5 F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363  
F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415  
F-HEMBA1001744//EST//8.7e-77 :420:92//Hs.133226:AI052250  
F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924  
F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328  
10 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:  
N41598  
F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622  
F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:  
AB007943  
F-HEMBA1001791  
15 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570  
F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817  
F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233  
F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.  
118164:AB007969  
20 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305  
F-HEMBA1001815  
F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.  
158174:U66561  
F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845  
25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:  
AF064244  
F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:  
AF071309  
F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078  
30 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.I55243:N70293  
F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324  
F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:  
AB014517  
F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121  
35 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922  
F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036  
F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.  
158095:AB007953  
40 F-HEMBA1001896  
F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346  
F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633  
F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:  
200:62//Hs.9573:AF027302  
45 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511  
F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141  
F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:  
855:99//Hs.154934:AF000145  
F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295  
50 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221  
F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882  
F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943  
F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360  
F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//  
55 Hs.25674:AF072242  
F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930  
F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708  
F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

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Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178  
F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732  
5 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100  
F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581  
F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487  
F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803 :W63582  
10 F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426  
F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907  
F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827  
F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057  
15 F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776  
F-HEMBA1002084  
F-HEMBA1002092  
F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832  
20 F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276  
F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973  
F-HEMBA1002119  
F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802  
F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393  
25 F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980  
F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263  
F-HEMBA1002151  
F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695  
F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976  
30 F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965  
F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590  
F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219  
F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245  
35 F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141  
F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363  
F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589  
F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970  
40 F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696  
F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767  
F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281  
F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957  
45 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394  
F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455  
F-HEMBA1002241  
F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887  
50 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936  
F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420  
F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445  
55 F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404  
F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710  
F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

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- F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
F-HEMBA10023481//EST//1.0e-19:285:70//Ms.121860:AA776692  
5 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563  
F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289  
F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561  
15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490  
F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783  
20 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133  
F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
F-HEMBA1002495  
25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972  
30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951  
F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219  
F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587  
40 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169  
F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351  
50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886  
F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
F-HEMBA1002651  
55 F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142  
F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

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F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497  
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368  
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457  
 5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164  
 F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221  
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924  
 10 F-HEMBA1002712  
 F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800  
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521  
 15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811 :AB007867  
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596  
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372  
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786  
 20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817  
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126  
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947  
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809  
 25 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392  
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326  
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756  
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938  
 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185  
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744  
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119  
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904  
 35 F-HEMBA1002833  
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550  
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823  
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730  
 40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429  
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679  
 F-HEMBA1002921  
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001  
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915  
 45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148  
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053  
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703  
 50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460  
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925  
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099  
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092  
 55 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828  
 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219  
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) //1.5e-37:247:89//Hs.188:L20971



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F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564  
F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525  
5 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219  
F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486  
F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080  
F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454  
F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003  
10 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514  
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182  
F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438  
F-HEMBA1003067  
15 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164  
F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865  
F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454  
F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461  
F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881  
20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721  
F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872  
F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721  
F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802  
25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575  
F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314  
F-HEMBA1003136  
F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279  
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670  
30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588  
F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740  
F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895  
35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523  
F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135  
F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412  
F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080  
F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765  
40 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784  
F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310  
F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012  
F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694  
45 F-HEMBA1003250  
F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292  
F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991  
F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020  
50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864  
F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867  
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662  
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:AB011109  
55 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912  
F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160  
F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

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F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872  
F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459  
F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254  
5 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328  
F-HEMBA1003330  
F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329  
F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmid R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092  
10 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159  
F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819  
F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637  
F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017  
F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552  
15 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488  
F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813  
F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959  
F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309  
F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546  
20 F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962  
F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696  
F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378  
F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632  
25 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578  
F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600  
F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443  
F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067  
F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811  
30 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559  
F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311  
F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833  
F-HEMBA1003556  
F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122  
35 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327  
F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113  
F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972  
F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546  
40 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232  
F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285  
F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405  
F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827  
45 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916  
F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782  
F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344  
F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954  
50 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750  
F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159  
F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591  
55 F-HEMBA1003640//ESTs//1.1e-11:267:661//Hs.34359:AI122791  
F-HEMBA1003645  
F-HEMBA1003646  
F-HEMBA1003656

F-HEMBA1003662  
 F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381  
 F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906  
 F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204  
 5 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]/1.6e-100:478:98//Hs.118866:AI017072  
 F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691  
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187  
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116  
 10 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995  
 F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760  
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317  
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921  
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839  
 15 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503  
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid  
 R31180//0.16:242:62//Hs.153325:AC005390  
 F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946  
 20 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984  
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920  
 F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]/1.7e-24:224:81//Hs.18171:AA524327  
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172  
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064  
 25 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815  
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239  
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108  
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721  
 30 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516  
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220  
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/3.8e-40:151:88//Hs.139007:H74314  
 F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167  
 35 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367  
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U52840  
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002  
 F-HEMBA1003880  
 40 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295  
 F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.2e-49:295:92//Hs.114673:W72675  
 F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236  
 F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097  
 45 F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875  
 F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389  
 F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562  
 F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]/0.0029:222:61//Hs.144236:W52380  
 F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055  
 50 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580  
 F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/2.1e-44:243:76//Hs.91146:N73230  
 F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567  
 F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965  
 55 F-HEMBA1003978  
 F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009  
 F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456  
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

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0.022:349:58//Hs.104640:AF000561  
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573  
 5 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.I5519:  
 AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930  
 F-HEMBA1004042//EST//0.00088:272:6//Hs.155763:AI312281  
 10 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.I62529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.  
 15 46328:D87942  
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.  
 20 46468:U45984  
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957  
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064  
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759  
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260  
 25 F-HEMBA1004143  
 F-HEMBA1004146  
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056  
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:  
 AB018341  
 30 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427  
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.  
 35 10092:AI189282  
 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040  
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748  
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514  
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.I63588:AI073878  
 F-HEMBA1004238  
 40 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571  
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522  
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.  
 56205:U96876  
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112  
 45 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:  
 AB014588  
 F-HEMBA1004272  
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444  
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331  
 50 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:  
 99//Hs.101766:AF022795  
 F-HEMBA1004289  
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484  
 55 F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047  
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314  
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367  
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

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F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612  
F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062  
F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888  
5 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606  
F-HEMBA1004341  
F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667  
F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968  
10 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376  
F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928  
F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800  
F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019  
15 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250  
F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818  
F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199  
F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:AI246426  
20 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531  
F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219  
F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080  
F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606  
25 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984  
F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450  
F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600  
F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431  
F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503  
30 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492  
F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800  
F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416  
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381  
35 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552  
F-HEMBA1004554  
F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331  
F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802  
F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825  
40 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238  
F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661  
F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370  
45 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606  
F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198  
F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178  
F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416  
50 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891  
F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780  
F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522  
F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083  
F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796  
55 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582  
F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141  
F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252  
F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235  
 25 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971  
 30 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 55 F-HEMBA1004972  
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

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F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548  
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560  
 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193  
 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381  
 20 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561  
 25 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547  
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144  
 40 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723  
 55 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581  
 F-HEMBA1005353//EST//5.4e-09:2-22:68//Hs.119508:AA485732  
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:

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AF071787  
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905  
F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.  
154069:U06452  
5 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053  
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448  
F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:  
N25951  
F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:  
10 AI033807  
F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513  
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347  
F-HEMBA1005411  
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:  
15 537:99//Hs.4854:AF041248  
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323  
F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687  
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783  
F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107  
20 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:  
L37368  
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503  
F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219  
F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:  
25 AF039694  
F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029  
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:  
AC004957  
F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635  
30 F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911  
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353  
F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.  
22767:N99220  
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//  
35 Hs.143551:AF048693  
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575  
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:  
AF057280  
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219  
40 F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.  
17035:AI080471  
F-HEMBA1005530  
F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:  
391:64//Hs.30250:AF055376  
45 F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461  
F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903  
F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257  
F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507  
F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:  
50 AB007932  
F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873  
F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538  
F-HEMBA1005582  
F-HEMBA1005583  
55 F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381  
F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA  
FORMS//0.54:439:591//Hs.2137:D49357  
F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323



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F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280  
5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845  
F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956  
F-HEMBA1005666  
F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142  
- F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
15 F-HEMBA1005680  
F-HEMBA1005685  
F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406  
F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697  
F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
25 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
30 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953  
F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984  
40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880  
45 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
F-HEMBA1005963  
F-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
50 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
F-HEMBA1006002  
F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151  
55 F-HEMBA1006031  
F-HEMBA1006035  
F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

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F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422  
 F-HEMBA1006081  
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788  
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313  
 5 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799  
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741  
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968  
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222  
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372  
 10 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734  
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881  
 F-HEMBA1006155  
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575  
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627  
 15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117  
 F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540  
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557  
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046  
 F-HEMBA1006252  
 20 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706  
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:  
 AB018341  
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631  
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140  
 25 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770  
 F-HEMBA1006283  
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964  
 F-HEMBA1006291  
 F-HEMBA1006293  
 30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//  
 Hs.46465:U45285  
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174  
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350  
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789  
 35 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142  
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.  
 22767:N99220  
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287  
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244  
 40 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026  
 F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.  
 80667:AF010233  
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:  
 265:61//Hs.8813:AF032922  
 45 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531  
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503  
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477  
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881  
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830  
 50 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835  
 F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264  
 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194  
 F-HEMBA1006445  
 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889  
 55 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369  
 F-HEMBA1006467  
 F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453  
 F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:

AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

5 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

10 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

15 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898

20 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778

25 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

30 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

35 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282

40 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

45 F-HEMBA1006676

F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198

F-HEMBA1006708

50 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

55 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

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F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-  
 SOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC  
 15 REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214  
 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065 :366:621//Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:  
 AJ010841  
 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.  
 14934:AF004828  
 F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89//  
 Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:  
 35 70//Hs.43003:AF035812  
 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:  
 M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:  
 57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.Se-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:641//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085  
 F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-  
 39:248:90//Hs.157148:AA311921  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

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F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:  
D86987  
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252  
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:  
5 AB018340  
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.  
82314:M31642  
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204  
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575  
10 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:  
U13695  
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836  
F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475  
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529  
15 F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637  
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062  
F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615  
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506  
F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634  
20 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241  
F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:  
W58370  
F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130  
F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006  
25 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561  
F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568  
F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073  
F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.  
83428:M58603  
30 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307  
F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392  
F-HEMBA1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z46788  
F-HEMBA1000036  
F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:  
35 98//Hs.20815:AF084928  
F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358  
F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319  
F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131  
F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717  
40 F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503  
F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923  
F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304  
F-HEMBA1000083  
F-HEMBA1000089//EST//0.0016:192:661//Hs.137093:AA917621  
45 F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645  
F-HEMBA1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627  
F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763  
F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521  
F-HEMBA1000136//ESTs//12.3e-101:507:96//Hs.12659:AA195207  
50 F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044  
F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881  
F-HEMBA1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715  
F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646  
F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457  
55 F-HEMBA1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:  
AB011129  
F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277  
F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013

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F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEMBB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483  
 5 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981//Hs.151411:AF075587  
 F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 10 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.109224:N46684  
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326  
 15 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 20 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:761//Hs.155464:AF088219  
 F-HEMBB1000341  
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 25 F-HEMBB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874  
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970  
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 30 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144  
 35 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEMBB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 40 F-HEMBB1000472  
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEMBB1000491  
 45 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products}//1.6e-46:409:77//Hs.102761:U25029  
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEMBB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 50 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/7.7e-31:554:67//Hs.157142:U85996  
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 55 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293  
 F-HEMBB1000564  
 F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

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F-HEM BB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEM BB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEM BB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 5 F-HEM BB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990  
 F-HEM BB1000592//EST//0.0038:51:88//Hs.148022:AI269323  
 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEM BB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589  
 F-HEM BB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEM BB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEM BB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481  
 F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEM BB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEM BB1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 15 F-HEM BB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEM BB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEM BB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEM BB1000665//EST//0.44:152:63//Hs.149534:AI280924  
 F-HEM BB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 20 F-HEM BB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEM BB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEM BB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEM BB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 25 F-HEM BB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703  
 F-HEM BB1000709//EST//0.99:110:651//Hs.162437:AA577510  
 F-HEM BB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEM BB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEM BB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 30 F-HEM BB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216  
 F-HEM BB1000763  
 F-HEM BB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEM BB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390  
 35 F-HEM BB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEM BB1000789//Homosapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577  
 F-HEM BB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEM BB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 40 F-HEM BB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEM BB1000810//ESTs//0.038:92:71//Hs.148763:AA66887  
 F-HEM BB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEM BB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEM BB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
 45 F-HEM BB1000827  
 F-HEM BB1000831  
 F-HEM BB1000835//EST//4.3e-27:201:851//Hs.141451:N29915  
 F-HEM BB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEM BB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503  
 50 F-HEM BB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEM BB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEM BB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
 55 F-HEM BB1000887  
 F-HEM BB1000888//ESTs//1.0:137:67//Hs.8121:AA521290  
 F-HEM BB1000890//ESTs//1.0:116:65//Hs.7105:T23433  
 F-HEM BB1000893//EST//0.0079:408:58//Hs.146504:AI129834

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F-HEM BB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
 F-HEM BB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEM BB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEM BB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
 5 F-HEM BB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEM BB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEM BB1000947  
 F-HEM BB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEM BB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 10 F-HEM BB1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEM BB1000981  
 F-HEM BB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEM BB1000991//EST//0.12:125:66//Hs.22945:R43713  
 15 F-HEM BB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055  
 F-HEM BB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEM BB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310  
 20 F-HEM BB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEM BB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEM BB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970  
 F-HEM BB1001037//EST//0.0057:192:66//Hs.149987:AI291177  
 25 F-HEM BB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721  
 F-HEM BB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEM BB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 30 F-HEM BB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942  
 F-HEM BB1001063  
 F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEM BB1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEM BB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 35 F-HEM BB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84:75//Hs.112434:U50529  
 F-HEM BB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEM BB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 40 F-HEM BB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEM BB1001119  
 F-HEM BB1001126  
 F-HEM BB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEM BB1001137  
 45 F-HEM BB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329  
 F-HEM BB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854  
 F-HEM BB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716  
 F-HEM BB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863  
 F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334  
 50 F-HEM BB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEM BB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129  
 F-HEM BB1001199  
 F-HEM BB1001208//ESTs//0.12:120:69//Hs.130093:AA928802  
 55 F-HEM BB1001209//EST//0.00028:215:65//Hs.118276:W15258  
 F-HEM BB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452  
 F-HEM BB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157  
 F-HEM BB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.



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158241:AB007976  
F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790  
F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754  
5 F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909  
F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219  
F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977  
F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828  
10 F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248  
F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:U13045  
F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021  
15 F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890  
F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848  
F-HEMBB1001302  
F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725  
20 F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339  
F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219  
F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503  
F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380  
F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222  
25 F-HEMBB1001335  
F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135  
F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694  
F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878  
30 F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142  
F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648  
F-HEMBB1001364  
F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347  
35 F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219  
F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973  
F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099  
F-HEMBB1001384  
40 F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230  
F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503  
F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988  
F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827  
45 F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174  
F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175  
F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345  
F-HEMBB1001443  
50 F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216  
F-HEMBB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038  
F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920  
F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220  
55 F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740  
F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303  
F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

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F-HEM BB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942

F-HEM BB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

F-HEM BB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735

5 F-HEM BB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093

F-HEM BB1001536//ESTs//0.0047:120:68//Hs.144858:R67748

F-HEM BB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306

F-HEM BB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//

10 Hs.102877:U41315

F-HEM BB1001562//ESTs//0.95:161:61//Hs.145075:AI208240

F-HEM BB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953

F-HEM BB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

15 F-HEM BB1001585

F-HEM BB1001586//EST//0.84:132:64//Hs.145264:AI218708

F-HEM BB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289

F-HEM BB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414

F-HEM BB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680

20 F-HEM BB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314

F-HEM BB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713

F-HEM BB1001635//ESTs//0.92:282:60//Hs.126980:AA934077

F-HEM BB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172

F-HEM BB1001641//EST//0.11:53:81//Hs.112445:AA594279

25 F-HEM BB1001653//EST//0.91:124:64//Hs.144213:T40480

F-HEM BB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407

F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:AI252519

F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546

30 F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496

F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430

F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664

F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398

35 F-HEM BB1001706

F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219

F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064

F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219

F-HEM BB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578

40 F-HEM BB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

F-HEM BB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144

F-HEM BB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

F-HEM BB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

45 F-HEM BB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976

F-HEM BB1001785//EST//0.16:262:60//Hs.162526:AA584102

F-HEM BB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

50 F-HEM BB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951

F-HEM BB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956

F-HEM BB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017

F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209

55 F-HEM BB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190

F-HEM BB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067

F-HEM BB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

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F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858  
 F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219  
 F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752  
 F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371  
 5 F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503  
 F-HEMBB1001872  
 F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478  
 F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743  
 10 F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868  
 F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEMBB1001905  
 F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155  
 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742  
 15 F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEMBB1001911  
 F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113  
 20 F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245  
 F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398  
 F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875  
 25 F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053  
 F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEMBB1001973//Myelin oligodendrocyte glycoprotein (alternative products)//2.1e-48:426:78//Hs.53217:Z48051  
 35 F-HEMBB1001983  
 F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEMBB1002044  
 F-HEMBB1002045  
 F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512  
 F-HEMBB1002069  
 F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 55 F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080  
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027  
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

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F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254  
 F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208  
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350  
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934  
 5 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332  
 F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813  
 F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219  
 F-HEMBB1002247  
 F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 10 6.8e-47:418:77//Hs.125231:AF068006  
 F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:  
 AB011166  
 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314  
 F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//  
 15 Hs.58169:AF017790  
 F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998  
 F-HEMBB1002300  
 F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.  
 46468:U45984  
 20 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083  
 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054  
 F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188  
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:  
 AJ010841  
 25 F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991  
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:  
 U00943  
 F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838  
 F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796  
 30 F-HEMBB1002381  
 F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566  
 F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784  
 F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456  
 F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.  
 35 159897:AB007970  
 F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150  
 F-HEMBB1002442  
 F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087  
 F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101  
 40 F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274  
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885  
 F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//  
 Hs.74304:AF001691  
 F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051  
 45 F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:  
 M89796  
 F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494  
 F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725  
 F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354  
 50 F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503  
 F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719  
 F-HEMBB1002531  
 F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219  
 F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102  
 55 F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648  
 F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191  
 F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286  
 F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

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F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749  
 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711  
 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811  
 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504  
 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922  
 25 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750  
 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281  
 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174  
 40 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792  
 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050  
 55 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695  
 F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

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F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.  
 158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:  
 98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:  
 117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME  
 III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:  
 AF061573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:  
 AF034546  
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:  
 AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:  
 93//Hs.9043:W21827  
 55 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete  
 cds//0.58:311:63//Hs.66721:D49818  
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

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F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete  
 cds//5.8e-51:404:80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
 15 cds//8.8e-45:390:78//Hs.159523:AF001622  
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494  
 20 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:  
 25 AF023674  
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:  
 K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:  
 U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//  
 Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:  
 AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.  
 158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:  
 AF100141  
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580  
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:  
 50 AB011147  
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:  
 Z48051  
 55 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//  
 9.8e-19:131:76//Hs.118972:AA761369  
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

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F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 10 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.  
 35 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968  
 55 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:  
 61//Hs.98384:AF062006  
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038



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F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178  
F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI19882  
F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719  
5 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503  
F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749  
10 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254  
15 F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627  
F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045  
F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915  
20 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
F-MAMMA1001133  
F-MAMMA1001139  
F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534  
F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217  
25 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147  
F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
F-MAMMA1001181  
30 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171  
F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
F-MAMMA1001198  
F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348  
35 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776  
F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087  
40 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534  
F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
F-MAMMA1001244  
F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476  
45 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561  
F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
50 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426  
55 F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305  
F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087  
 F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147  
 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806  
 F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197  
 5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267  
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258  
 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981  
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR//4.6e-09:415:58//Hs.839:M86826  
 10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402  
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763  
 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928  
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394  
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.  
 15 46328:D87942  
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108  
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321  
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590  
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040  
 20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053  
 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:  
 D78335  
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:  
 AA524909  
 25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366  
 F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269  
 F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795  
 F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506  
 F-MAMMA1001547  
 30 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:  
 AB007931  
 F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:  
 AI017072  
 F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764  
 35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339  
 F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132  
 F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375  
 F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266  
 F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152  
 40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727  
 F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc  
 Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-  
 67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger  
 protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and  
 45 DXS1055//1.4e-40:447:73//Hs.154353:AL022165  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796  
 F-MAMMA1001635  
 F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524  
 F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:  
 50 68//Hs.59829:AB014602  
 F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:  
 AB007917  
 F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 55 F-MAMMA1001671  
 F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317  
 F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889  
 F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

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F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549  
F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984  
5 F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548  
F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926  
F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634  
F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098  
F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768  
10 F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245  
F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503  
F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632  
F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822  
15 F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109  
F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.102576:AJ010230  
F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072  
F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832  
20 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080  
F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:U38276  
F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940  
25 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549  
F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:K00627  
F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869  
F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987  
30 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884  
F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096  
F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582  
F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589  
F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293  
35 F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742  
F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691  
F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827  
40 F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665  
F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028  
F-MAMMA1001854  
F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218  
F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060  
45 F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209  
F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687  
F-MAMMA1001878  
F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944  
50 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576  
F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078  
F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521  
F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874  
F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529  
55 F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859  
F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317  
F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878  
F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:

N91115

F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915

F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159

F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.158095:AB007953

F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580

F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225

F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256

F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305

F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503

F-MAMMA1002078

F-MAMMA1002082

F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012

F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:AJ010840

F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932

F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219

F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963

F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638

F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338

F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837

F-MAMMA1002153

F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385

F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999

F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206

F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172

F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935

F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776

F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481

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F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956  
F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291  
F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908  
5 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536  
F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515  
F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026  
F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:  
10 K00627  
F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254  
F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633  
F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591  
15 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907  
F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086  
F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539  
F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901  
20 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733  
F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818  
F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830  
F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923  
F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345  
25 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677  
F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022  
F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362  
F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624  
F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632  
30 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737  
F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745  
F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788  
F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030  
F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087  
35 F-MAMMA1002446  
F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809  
F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707  
F-MAMMA1002470  
40 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779  
F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059  
F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460  
45 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628  
F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920  
F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392  
F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//  
50 4.5e-162:775:97//Hs.18858:AF065214  
F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788  
F-MAMMA1002554  
F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822  
F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421  
55 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368  
F-MAMMA1002573//ESTs//2.1e-4.8:265:94//Hs.155128:AI224516  
F-MAMMA1002585  
F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

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F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107  
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958  
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220  
 5 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895:AA428463  
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357  
 F-MAMMA1002618  
 F-MAMMA1002619  
 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449  
 10 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300  
 F-MAMMA1002625  
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.158241:AB007976  
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:AB006626  
 15 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335  
 20 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:D86987  
 25 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915  
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697  
 30 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165  
 35 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312  
 F-MAMMA1002748  
 40 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902  
 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293  
 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782  
 F-MAMMA1002769  
 45 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563  
 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988  
 F-MAMMA1002782  
 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710  
 50 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919  
 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514  
 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:AB011135  
 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067  
 55 F-MAMMA1002835  
 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951  
 F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

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F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:AB018353

F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:AI357868

F-MAMMA1002858

5 F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643

F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284

F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423

F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632

10 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:D45027

F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270

F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657

F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666

F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265

15 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658

F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952

F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125

F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730

F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.102928:AI346344

20 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:AB014598

F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389

F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418

25 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884

F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400

F-MAMMA1002972

F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932

F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944

30 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645

F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931

F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.159897:AB007970

F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979

35 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:AF054174

F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372

F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062

F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951

40 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137

F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549

F-MAMMA1003035

F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391

F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750

45 F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639

F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336

F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742

F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518

50 F-MAMMA1003056

F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.96500:AI206781

F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618

F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531

55 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045

F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

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F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634  
F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:  
AF105424  
F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786  
5 F-MAMMA1003140  
F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062  
F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:  
AB011087  
F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632  
10 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204  
F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886  
F-NT2RM1000032  
F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782  
F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:  
15 AB014590  
F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204  
F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067  
F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//  
Hs.46465:U45285  
20 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210  
F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472  
F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:  
AB014561  
F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689  
25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:  
AF007155  
F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054  
F-NT2RM1000127  
F-NT2RM1000131  
30 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene en-  
coding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959  
F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.  
110099:AB010419  
35 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:  
AF007155  
F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:A1424382  
F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458  
F-NT2RM1000242  
F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:  
40 135:66//Hs.27910:AF049105  
F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190  
F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516  
F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:  
A1037879  
45 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920  
F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047  
F-NT2RM1000272  
F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:  
73//Hs.15071:AA781144  
50 F-NT2RM1000300  
F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880  
F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205  
F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976  
F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:A1125798  
55 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608  
F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691  
F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.  
163707:AA137181



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F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507  
F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353  
F-NT2RM1000399  
F-NT2RM1000421  
5 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//  
Hs.20815:AF084928  
F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382  
F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660  
F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847  
10 F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957  
F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204  
F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625  
F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.ele-  
gans]//6.2e-51:254:98//Hs.132096:AA314601  
15 F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:  
AF038957  
F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297  
F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279  
F-NT2RM1000672  
20 F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348  
F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101  
F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706  
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832  
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:  
25 AB011139  
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208  
F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465  
F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885  
F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 :  
30 U39067  
F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503  
F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845  
F-NT2RM1000800  
F-NT2RM1000802  
35 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208  
F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957  
F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422  
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726  
F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148  
40 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:  
AJ010840  
F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643  
F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619  
F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239  
45 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
gene//4.0e-155:750:97//Hs.132898:AC004770  
F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.  
26285:AF082516  
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:  
50 AB014561  
F-NT2RM1000894  
F-NT2RM1000898  
F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701  
F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679  
55 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350  
F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440  
F-NT2RM1000978  
F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//

Hs.58488:U97067  
 F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200  
 F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395  
 F-NT2RM1001044//ESTs, Weakly similar to C43E11.9[C.elegans]//3.0e-98:491:96//Hs.102173:AA045270  
 5 F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204  
 F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703  
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822  
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846  
 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198  
 10 F-NT2RM1001085  
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244  
 F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331  
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564  
 F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495  
 15 F-NT2RM1001115  
 F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074  
 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113  
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563  
 F-NT2RM2000030  
 20 F-NT2RM2000032//ESTs//7.1 e-18:138:68//Hs.114031:AA700958  
 F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243  
 F-NT2RM2000092  
 F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085  
 F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428  
 25 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767  
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:  
 97//Hs.18953:AF067223  
 F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999  
 F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672  
 30 F-ntnnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328  
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:  
 AB011162  
 F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520  
 F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500  
 35 F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981  
 F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127  
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:  
 AB011132  
 F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543  
 40 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//  
 Hs.75871:U48251  
 F-NT2RM2000371  
 F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866  
 F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698  
 45 F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006  
 F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582  
 F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053  
 F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//  
 Hs.553:L05568  
 50 F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379  
 F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807  
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290  
 F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.  
 76669:U08021  
 55 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812:  
 AF061243  
 F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487  
 F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:

AI141736  
 F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220  
 F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108  
 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508  
 5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128  
 F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [*Saccharomyces cerevisiae*]//1.4e-33:214:92//Hs.55609:W37993  
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987  
 10 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220  
 F-NT2RM2000594  
 F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963  
 F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313  
 15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548  
 F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093  
 F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258  
 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272  
 20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558  
 F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702  
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576  
 F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371  
 25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083  
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984  
 F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342  
 F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244  
 30 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [*Saccharomyces cerevisiae*]//4.2e-85:464:91//Hs.161551:W24286  
 F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750  
 F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338  
 F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701  
 35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046  
 F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [*D.melanogaster*]//6.2e-94:441:99//Hs.59075:AI023761  
 F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433  
 40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831  
 F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [*Saccharomyces cerevisiae*]//2.9e-48:282:93//Hs.17035:AI080471  
 F-NT2RM2001065  
 F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258  
 45 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153  
 F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190  
 F-NT2RM2001141  
 50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042  
 F-NT2RM2001177  
 F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [*C.elegans*]//2.4e-23:149:93//Hs.10618:AI288739  
 F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959  
 F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630  
 55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349  
 F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766  
 F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928  
 F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

AF039694  
 F-NT2RM2001256  
 F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845  
 F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601  
 5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615  
 F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:  
 AI138605  
 F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567  
 F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706  
 10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905  
 F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322  
 F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382  
 F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378  
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:  
 15 AJ007509  
 F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303  
 F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903  
 F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969  
 F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459  
 20 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262  
 F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:  
 64//Hs.1042:M62800  
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077  
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902  
 25 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729  
 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431  
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918  
 30 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:  
 AB014518  
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952  
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//  
 Hs.22142:AA814725  
 35 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301  
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-  
 40 173:802:99//Hs.31323:AF044195  
 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:  
 671:97//Hs.27721:U17907  
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:  
 AB011129  
 45 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356  
 F-NT2RM2001675  
 F-NT2RM20016811//ESTs//0.16:197:63//Hs.20585:R10305  
 F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216  
 50 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937  
 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415  
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817  
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//  
 0.95:270:61//Hs.15791:AF027826  
 55 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788  
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650  
 F-NT2RM2001718  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

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F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931

F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132

5 F-NT2RM2001743

F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399

F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742

10 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933

F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698

F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595

F-NT2RM2001785//Homo sapiens chromosome 11, BAC ClT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

20 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080

25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610

30 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931

F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840

35 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080

40 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392

F-NT2RM2001982

F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816

F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778

45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538

F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398

F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274

F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729

F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516

50 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427

F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154

F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377

F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840

55 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435

F-NT2RM2002128

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F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274  
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928  
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:AB007936  
 5 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.99936:X14487  
 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563  
 F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074  
 10 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464  
 F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674  
 F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511  
 F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H. sapiens]//1.6e-30:369:70//Hs.114623:AI204280  
 15 F-NT2RM4000086  
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865  
 F-NT2RM4000139  
 F-NT2RM4000155  
 20 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632  
 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853  
 F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044  
 F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190  
 25 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744  
 F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147  
 F-NT2RM4000200  
 F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:AB006626  
 30 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:AB018255  
 F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651  
 F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458  
 35 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582  
 F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439  
 F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.93841:AA442297  
 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.46328:D87942  
 40 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.31305:M99438  
 F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:AB000712  
 45 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707  
 F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.12796:W27884  
 F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630  
 F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:M023761  
 50 F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425  
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542  
 F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745  
 F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718  
 55 F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

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F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046  
F-NT2RM4000421  
5 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166  
F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820  
F-NT2RM4000457  
F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631//Hs.66369:U95040  
10 F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004  
F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632  
F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915  
F-NT2RM4000514  
F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409  
15 F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305  
F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967  
F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987  
F-NT2RM4000534  
20 F-NT2RM4000585  
F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938  
F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227  
25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390  
F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068  
F-NT2RM4000616  
F-NT2RM4000674  
F-NT2RM4000689  
30 F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529  
F-NT2RM4000700  
F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789  
F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181  
35 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605  
F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:AB018303  
F-NT2RM4000741  
40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.112361:R99396  
F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815  
F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731  
F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:AB007920  
45 F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186  
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306  
F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:AI337820  
50 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676  
F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301  
F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387  
F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568  
55 F-NT2RM4000833  
F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322  
F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934  
F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapiens]

ens//4.4e-29:164:95//Hs.115095:AI392943  
F-NT2RM4000887  
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete  
cgs//6.8e-22:407:64//Hs.21293:AB011004  
5 F-NT2RM4000950  
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546  
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875  
F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926  
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:  
10 AB018272  
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:  
AB014539  
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:  
AB018254  
15 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:  
AI247543  
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//  
0.79:142:69//Hs.77424:M63835  
F-NT2RM4001084  
20 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758  
F-NT2RM4001116  
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701  
F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730  
F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145  
25 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351  
F-NT2RM4001187  
F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220  
F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933  
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.  
30 14934:AF004828  
F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME  
III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205  
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70//  
Hs.104925:AF059611  
35 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.  
26676:AA033997  
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:  
AB007950  
F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003  
40 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973  
F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335  
F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016  
F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988  
F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTER-  
GENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714  
45 F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7  
protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818  
F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656  
F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:  
50 AF098799  
F-NT2RM4001384  
F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575  
F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520  
F-NT2RM4001412  
55 F-NT2RM4001414//ESTs, Moderately similar to 18547\_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817  
F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087  
F-NT2RM4001444  
F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658



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F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914  
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784  
 5 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585  
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619  
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247  
 F-NT2RM4001557  
 10 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487  
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453  
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859  
 F-NT2RM4001582  
 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566  
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094  
 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077  
 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334  
 20 F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739  
 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946  
 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339  
 25 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320  
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323  
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638  
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957  
 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905  
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903  
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318  
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306  
 F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719  
 35 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270  
 40 F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677  
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105  
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547  
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712  
 45 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442  
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687  
 F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824  
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204  
 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814  
 F-NT2RM4001856  
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711  
 55 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984  
 F-NT2RM4001880  
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

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F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633  
F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875  
F-NT2RM4001938  
5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162  
F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087  
F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493  
10 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862  
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341  
F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082  
F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936  
15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271  
F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601  
F-NT2RM4002034  
F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048  
F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912  
20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540  
F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802  
F-NT2RM4002063  
25 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309  
F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040  
F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302  
F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569  
30 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.146459:X66975  
F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743  
35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542  
F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877  
F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158  
F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879  
40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535  
F-NT2RM4002174  
F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998  
F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276  
45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454  
F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182  
F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984  
F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966  
50 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764  
F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118  
F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180  
F-NT2RM4002281  
F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979  
55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457  
F-NT2RM4002301  
F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331  
F-NT2RM4002339

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F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454  
F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549  
5 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263  
F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293  
F-NT2RM4002390  
F-NT2RM4002398  
F-NT2RM4002409  
10 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.26676:AA033997  
F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151  
F-NT2RM4002452  
F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783  
F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780  
15 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255  
F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591  
F-NT2RM4002493  
20 F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347  
F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219  
F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020  
F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075  
25 F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor All/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176  
F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004  
F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273  
30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054  
F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394  
F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151  
F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275  
35 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402  
F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587  
F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449  
40 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907  
F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647  
F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834  
F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924  
45 F-NT2RP1000111  
F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699  
F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025  
F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901  
50 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792  
F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430  
F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535  
F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499  
55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703  
F-NT2RP1000243  
F-NT2RP1000259  
F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.

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4214:AF067730  
F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661  
F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551  
5 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231  
F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204  
F-NT2RP1000357  
F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807  
10 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538  
F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594  
F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031  
15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159  
F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.3e-177:857:97//Hs.6823:W18181  
F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815  
20 F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603  
F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862  
F-NT2RP1000460  
F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985  
25 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634  
F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102  
F-NT2RP1000493  
30 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977  
F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992  
F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098  
F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418  
35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213  
F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385  
F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770  
F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475  
40 F-NT2RP1000630  
F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576  
F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553  
45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736  
F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148  
F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612  
F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045  
50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644  
F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434  
F-NT2RP1000746  
F-NT2RP1000767  
55 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023  
F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401  
F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

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2.7e-23:147:91//Hs.102336:Z83838  
F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:  
96//Hs.18953:AF067223  
5 F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903  
F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990  
F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838  
F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875  
F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023  
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094  
10 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683  
F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847  
F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94//  
Hs.122153:AA780270  
F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248  
15 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400  
F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:  
185:87//Hs.108332:U39317  
F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803  
F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847  
20 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885  
F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858  
F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866  
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435  
F-NT2RP1001011  
25 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163  
F-NT2RP1001014  
F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764  
F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901  
F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531  
30 F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845:  
AF032886  
F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293:  
95//Hs.32751:H38087  
F-NT2RP1001173  
35 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:  
AF054174  
F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524  
F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150  
F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.  
40 25195:U81523  
F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094  
F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:  
AJ002231  
F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724  
45 F-NT2RP1001294  
F-NT2RP1001302  
F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341  
F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815  
F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
50 gene//3.1e-87:437:97//Hs.132898:AC004770  
F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-  
rus]//6.8e-101:480:94//Hs.75017:AA166853  
F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859  
F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673  
55 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081  
F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

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F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
 F-NT2RP1001466  
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
 F-NT2RP1001482  
 5 F-NT2RP1001494  
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400  
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277  
 F-NT2RP1001569  
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913  
 10 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081  
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390  
 15 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763  
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359  
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290  
 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749  
 F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433  
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134  
 25 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609  
 30 F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078  
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338  
 35 F-NT2RP2000091  
 F-NT2RP2000097  
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963  
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390  
 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356  
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177  
 45 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195  
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475  
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910  
 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291  
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713  
 55 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208

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F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462  
F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990  
5 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669  
F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378  
F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719  
F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846  
F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691  
F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011  
10 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599  
F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910  
F-NT2RP2000288  
F-NT2RP2000289  
F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.37138:U35376  
15 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467  
F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381  
F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006  
20 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905  
F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:X60673  
F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547  
F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981  
25 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530  
F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047  
F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010  
F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779:AA626790  
30 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265  
F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381  
F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918  
35 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747  
F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293  
F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702  
F-NT2RP2000510  
F-NT2RP2000516  
40 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA806768  
F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144  
F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656  
45 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514  
F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174  
F-NT2RP2000656  
F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602  
F-NT2RP2000668  
50 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453  
F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442  
F-NT2RP2000710  
F-NT2RP2000715  
55 F-NT2RP2000731  
F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242  
F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739

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F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182  
 5 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.  
 75794:U80811  
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850  
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I  
 [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:  
 AB018284  
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65//  
 15 Hs.46146:AA418097  
 F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266  
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014  
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:  
 20 AB018298  
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494  
 F-NT2RP2000970  
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700  
 25 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944  
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292  
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117  
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.  
 67619:AB007957  
 30 F-NT2RP2001065  
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-NT2RP2001081  
 F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560  
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219  
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191  
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:  
 201:91//Hs.118470:AI336362  
 F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582  
 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361  
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:  
 AB007949  
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011  
 F-NT2RP2001196  
 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598  
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053  
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367  
 F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813  
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353  
 F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277  
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412  
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287  
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387  
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783  
 F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522  
 55 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883  
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244  
 F-NT2RP2001378  
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558



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F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:  
 225:62//Hs.159402:AC005609  
 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767  
 F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088  
 5 F-NT2RP2001420  
 F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018  
 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875  
 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966  
 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//  
 10 9.8e-56:603:72//Hs.75544:Z82248  
 F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218  
 F-NT2RP2001449  
 F-NT2RP2001450  
 F-NT2RP2001467  
 15 F-NT2RP2001506  
 F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779  
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:  
 Y14494  
 F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134  
 20 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 5.2e-105:384:94//Hs.99742:AF035586  
 F-NT2RP2001560  
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.  
 67619:AB007957  
 25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389  
 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876  
 F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268  
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:  
 AB018340  
 30 F-NT2RP2001613  
 F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229  
 F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//  
 Hs.58488:U97067  
 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-  
 35 NA, complete cds//1.3e-145:687:97//Hs.159558:AF058718  
 F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328  
 F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936  
 F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314  
 F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 :  
 40 U52840  
 F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091  
 F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:  
 AI197870  
 F-NT2RP2001721  
 45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991  
 F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstrans-  
 ferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697  
 F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete\_cds//5.2e-34:191:96//Hs.47504:  
 AF091754  
 50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180  
 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250  
 F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610  
 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:  
 AF027219  
 55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768  
 F-NT2RP2001883  
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:  
 90//Hs.142189:M74161

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F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650  
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757  
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754  
 F-NT2RP2001936  
 5 F-NT2RP2001943  
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797  
 F-NT2RP2001947  
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489  
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892  
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:  
 AB011117  
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:  
 AB018299  
 15 F-NT2RP2002032  
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543  
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336  
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509  
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198  
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284  
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:  
 66//Hs.44553:AF055634  
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183  
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014  
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:  
 AJ007509  
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.  
 30 122755:AF032986  
 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286  
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363  
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112  
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314  
 35 F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:  
 C06057  
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:  
 M58460  
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//  
 40 6.8e-15:228:67//Hs.111323:AF077954  
 F-NT2RP2002208  
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628  
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318  
 F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439  
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:  
 AF005418  
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720  
 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373  
 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.  
 24812:AF069532  
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445  
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:  
 55 95//Hs.31034:AB015594  
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637  
 F-NT2RP2002373  
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

97//Hs.109051:AF038958  
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289  
 F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433  
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098  
 5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326  
 F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265  
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436  
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045  
 10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929  
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289  
 F-NT2RP2002498  
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044  
 15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334  
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212  
 F-NT2RP2002537  
 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096  
 20 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979  
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341  
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309  
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503  
 25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082  
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805  
 F-NT2RP2002621  
 30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317  
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493  
 F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385  
 35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583  
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572  
 F-NT2RP2002727  
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217  
 40 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297  
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016  
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329  
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709  
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705  
 45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204  
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407  
 F-NT2RP2002800  
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763  
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142  
 50 F-NT2RP2002862  
 F-NT2RP2002880  
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573  
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392  
 55 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517  
 F-NT2RP2002939  
 F-NT2RP2002954

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F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317  
F-NT2RP2002979  
F-NT2RP2002980  
5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569  
F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740  
F-NT2RP2002993  
F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219  
10 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741  
F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019  
F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190  
F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050  
15 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633  
F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379  
F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161  
F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544  
20 F-NT2RP2003137  
F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520  
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025  
F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170  
25 F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944  
F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353  
F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123  
F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223  
F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594  
30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794  
F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947  
F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696  
F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153  
35 F-NT2RP2003265  
F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:C06057  
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525  
40 F-NT2RP2003280  
F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159  
F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334  
45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572  
F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312  
F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752  
F-NT2RP2003308  
50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227  
F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765  
F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963  
F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108  
55 F-NT2RP2003391  
F-NT2RP2003393  
F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023  
F-NT2RP2003401

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F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/3.7e-33:303:77//Hs.14038:R06800  
F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893  
F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647  
5 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320  
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770  
F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106  
F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136  
10 F-NT2RP2003506  
F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803  
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270  
F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783  
15 F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019  
F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765  
F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010  
F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513  
F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800  
20 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931  
F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947  
F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]/1.3e-63:224:95//Hs.34627:AA126463  
25 F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067  
F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166  
F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252  
30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006  
F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875  
F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247  
F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561  
35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]/5.1e-44:269:91//Hs.139757:N95271  
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097  
F-NT2RP2003713  
F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180  
40 F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879  
F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318  
F-NT2RP2003751  
45 F-NT2RP2003760  
F-NT2RP2003764  
F-NT2RP2003769  
F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677  
F-NT2RP2003777  
50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]/3.7e-63:356:92//Hs.16131:AA568689  
F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955  
F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742  
F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368  
F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425  
55 F-NT2RP2003859  
F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780  
F-NT2RP2003885  
F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]/2.2e-

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113:632:92//Hs.50072:AI378221  
 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296  
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458  
 5 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916  
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347  
 F-NT2RP2003984  
 10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036  
 F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369  
 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:AI380378  
 F-NT2RP2004014  
 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573  
 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942  
 20 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828  
 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292  
 F-NT2RP2004142  
 F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872  
 25 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666  
 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966  
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501  
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:AA626790  
 30 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317  
 F-NT2RP2004196  
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756  
 F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270  
 35 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756  
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680  
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536  
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487  
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:N25951  
 40 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263  
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544  
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416  
 45 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735  
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510  
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632  
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202  
 50 F-NT2RP2004365  
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986  
 F-NT2RP2004373  
 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916  
 55 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588  
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164  
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

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F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367  
 F-NT2RP2004412  
 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944  
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687  
 5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//0.45:  
 208:61//Hs.24040:AF006823  
 F-NT2RP2004490  
 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203  
 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//  
 10 Hs.73614:U83460  
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:  
 AB011163  
 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891  
 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:  
 15 AF039694  
 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219  
 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309  
 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898  
 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895  
 20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:  
 273:93//Hs.12845:N28835  
 F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908  
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291  
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:  
 25 AB007929  
 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839  
 F-NT2RP2004681  
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:  
 AB014525  
 30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942  
 F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780  
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:  
 AB007947  
 F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242  
 35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183  
 F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//  
 3.7e-110:548:96//Hs.85768:W16504  
 F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.  
 107474:AF045451  
 40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:  
 L40157  
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 4.9e-118:594:95//Hs.40820:AF058953  
 F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043  
 45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:  
 AF054179  
 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161  
 F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258  
 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111  
 50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144  
 F-NT2RP2004936  
 F-NT2RP2004959  
 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763  
 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478  
 55 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735  
 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927  
 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.  
 41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//  
 Hs.124161:AF065164  
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:  
 AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200  
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141  
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600  
 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433  
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067  
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035  
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612  
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:  
 15 AF055917  
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:  
 AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.  
 20 100555:X98743  
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803  
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:  
 AF045583  
 25 F-NT2RP2005147  
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582  
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:  
 AJ007509  
 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189  
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783  
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439  
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341  
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.  
 81452:AF030555  
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932  
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//  
 Hs.27007:AF060219  
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590  
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:  
 AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.  
 45 1569:U11701  
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds//0.016:353:62//Hs.113265:AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138  
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958  
 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:  
 489:96//Hs.107254:AC005943  
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122  
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.  
 113252:U80761  
 55 F-NT2RP2005407  
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133  
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068  
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164



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F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-  
rus]/8.5e-48:295:90//Hs.75017:AA166853  
F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243  
F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656  
5 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412  
F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:  
AB018315  
F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573  
F-NT2RP2005491  
10 F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164  
F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324  
F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:  
M64930  
F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669  
15 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:  
291:59//Hs.89709:L35546  
F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:  
444:92//Hs.119023:AF092563  
F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:  
20 AB018307  
F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]/3.5e-50:366:83//Hs.  
61833:AA036735  
F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:  
AJ012449  
25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:  
AB007963  
F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME  
III [C.elegans]/2.5e-51:292:93//Hs.105684:H24407  
F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822  
30 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839  
F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436  
F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627  
F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071  
F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085  
35 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702  
F-NT2RP2005635  
F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905  
F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145  
F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440  
40 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917  
F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:  
AB006626  
F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239  
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//  
45 Hs.25664:AF089814  
F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702  
F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836  
F-NT2RP2005694  
F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496:  
50 55//Hs.79326:L76703  
F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:  
AB018342  
F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527  
F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367  
55 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017  
F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191  
F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086  
F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769

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F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//  
 Hs.159651:AF068868  
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.  
 5 26285:AF082516  
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853  
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836  
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:  
 10 Z50115  
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556  
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.  
 34853:U28368  
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820  
 15 F-NT2RP2005812  
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595  
 F-NT2RP2005835  
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//  
 Hs.59829:AB014602  
 20 F-NT2RP2005853  
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:  
 98//Hs.50758:AF092564  
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567  
 F-NT2RP2005868  
 25 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:  
 L16782  
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943  
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360  
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399  
 30 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:  
 AA292186  
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770  
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339  
 F-NT2RP2006023  
 35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382  
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664  
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093  
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469  
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416  
 40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970  
 F-NT2RP2006100  
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135  
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349  
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240  
 45 F-NT2RP2006166  
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910  
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:  
 AB014554  
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:  
 50 AB018315  
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484  
 F-NT2RP2006237  
 F-NT2RP2006238  
 55 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970  
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630  
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:  
 60//Hs.75111:D87258

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F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262  
F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.36794:AI038407  
F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371  
5 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344  
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974  
F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174  
F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501  
10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341  
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734  
F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934  
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509  
15 F-NT2RP2006456  
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266  
F-NT2RP2006467  
F-NT2RP2006472  
F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048  
20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134  
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966  
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029  
25 F-NT2RP2006573  
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223  
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180  
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972  
30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560  
F-NT2RP3000047  
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376  
35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961  
F-NT2RP3000068  
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769  
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670  
F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608  
40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140  
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595  
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189  
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164  
45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503  
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961  
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779  
F-NT2RP3000207  
50 F-NT2RP3000220  
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569  
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740  
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972  
55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733  
F-NT2RP3000252  
F-NT2RP3000255  
F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

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F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821  
F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863  
5 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153  
F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242  
F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097  
10 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390  
F-NT2RP3000348  
F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754  
F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673  
15 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921  
F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016  
F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639  
F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873  
20 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185  
F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503  
F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948  
F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487  
25 F-NT2RP3000441  
F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562  
F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705  
F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068  
F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822  
F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058  
30 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667  
F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379  
F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966  
F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308  
F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412  
35 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404  
F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723  
F-NT2RP3000578  
F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277  
40 F-NT2RP3000584  
F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904  
F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914  
F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811  
F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492  
45 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980  
F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203  
F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683  
F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162  
F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333  
F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904  
50 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219  
F-NT2RP3000661  
F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789  
F-NT2RP3000685  
55 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001  
F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884  
F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854  
F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

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F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765  
F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937  
F-NT2RP3000815  
5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132  
F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700  
F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476  
F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012  
10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630  
F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520  
F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219  
F-NT2RP3000852  
15 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918  
F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476  
F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445  
F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204  
20 F-NT2RP3000875  
F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101  
F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374  
F-NT2RP3000917  
F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277  
25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407  
F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212  
F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411  
F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198  
F-NT2RP3001007  
30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707  
F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:AI244662  
F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219  
35 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325  
F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:AJ006470  
F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969  
40 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050  
F-NT2RP3001111  
F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088  
F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023  
F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779  
45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384  
F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367  
F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318  
F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297  
50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305  
F-NT2RP3001147  
F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605  
F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266  
F-NT2RP3001176  
55 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859  
F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981  
F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866  
F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

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F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756  
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237  
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132  
 F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109  
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:  
 AB018269  
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:  
 72//Hs.41728:L75847  
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566  
 10 F-NT2RP3001274  
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457  
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:  
 U44060  
 15 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type III)//0.012:522:56//Hs.904:U84010  
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966  
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:  
 20 AB007920  
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:  
 61//Hs.124161:AF065164  
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//  
 1.1e-81:421:96//Hs.32508:H29831  
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487  
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022  
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451  
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332  
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595  
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783  
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:  
 66//Hs.41728:L75847  
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.  
 111024:L77567  
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658  
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP3001426  
 F-NT2RP3001427  
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397  
 40 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-  
 05:195:65//Hs.115868:AA568393  
 F-NT2RP3001447  
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508  
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212  
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:  
 AF072836  
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877  
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
 2.8e-172:804:98//Hs.28285:AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:  
 91//Hs.85283:U36500  
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.  
 105912:AI431328  
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074  
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302  
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686:  
 M69013  
 5 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:  
 AF057280  
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688  
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349  
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435  
 F-NT2RP3001629  
 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149  
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:  
 AJ012449  
 15 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027  
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]/9.0e-53:  
 375:85//Hs.41127:AA555184  
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071  
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 20 [*Caenorhabditis elegans*]/4.0e-111:518:99//Hs.20364:AI420022  
 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198  
 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329  
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219  
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [*D.mela-*  
 25 *nogaster*]/1.4e-31:191:94//Hs.131279:AA486291  
 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862  
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]  
 //7.6e-159:747:98//Hs.6823:W18181  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:  
 30 565:97//Hs.159273:AF054177  
 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III  
 [*Caenorhabditis elegans*]/3.5e-116:554:98//Hs.144332:AA046836  
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918  
 F-NT2RP3001739  
 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172  
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete  
 cds//0.10:528:56//Hs.22138:U49250  
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:  
 U27193  
 40 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.  
 57783:U78525  
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:  
 AB007928  
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532  
 45 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361  
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162  
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634  
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729  
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:  
 50 U68727  
 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706  
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [*C.elegans*]/2.9e-94:452:98//Hs.54952:  
 AA872675  
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326  
 55 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896  
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185  
 F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247  
 F-NT2RP3001931

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F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398  
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:  
 AB014575  
 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335  
 5 F-NT2RP3001969  
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180  
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219  
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779  
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946  
 10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821  
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153  
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:  
 AA993745  
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155  
 15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:  
 407:97//Hs.131888:AI091806  
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503  
 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710  
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//  
 20 0.91:194:65//Hs.1298:J03779  
 F-NT2RP3002081  
 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:  
 297:61//Hs.102732:U88153  
 F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256  
 25 F-NT2RP3002108  
 F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018  
 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260  
 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with  
 some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative  
 30 CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009  
 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644  
 F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985  
 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //3.0e-61:340:93//Hs.11379:AA594140  
 35 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046  
 F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
 III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915  
 F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643  
 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:  
 40 242:57//Hs.114001:Z20656  
 F-NT2RP3002248  
 F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261  
 F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.  
 110637:AC004080  
 45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139  
 F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386  
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910  
 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871  
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383  
 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:  
 588:75//Hs.154672:X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:  
 Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200  
 55 F-NT2RP3002399  
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:  
 AB014578



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F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310  
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108  
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.  
 5 57738:U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:  
 AB018272  
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.  
 96759:AA469984  
 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706  
 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054  
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919  
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508  
 F-NT2RP3002603  
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888  
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900  
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.  
 20 151518:U38847  
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308  
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//  
 Hs.41086:AI337400  
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991  
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584  
 F-NT2RP3002687  
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200  
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657  
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514  
 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291  
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//  
 Hs.129736:AF040753  
 F-NT2RP3002785  
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713  
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:  
 AF004715  
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070  
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582  
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895  
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314  
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765  
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//  
 45 Hs.3826:U69560  
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:  
 AB011160  
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262  
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870  
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997  
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703  
 F-NT2RP3002985//Human TFIIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:  
 U28838  
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308  
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083  
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446  
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749  
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

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F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928  
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079  
 F-NT2RP3003078  
 F-NT2RP3003101  
 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:  
 88:68//Hs.99715:AA292700  
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740  
 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1)  
 mRNA, complete cds//0.013:438:57//Hs.101299:AF017061  
 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975  
 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:  
 63//Hs.118397:AF053944  
 F-NT2RP3003150  
 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.  
 15 37138:U35376  
 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093  
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933  
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854  
 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308  
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325  
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525  
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:  
 D44497  
 25 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:  
 AF055460  
 F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200  
 F-NT2Rp3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//  
 Hs.620:M69225  
 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:  
 AF044924  
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983  
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953  
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947  
 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503  
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947  
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058  
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200  
 F-NT2RP3003330  
 40 F-NT2RP3003344  
 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339  
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833  
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542  
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791  
 45 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363  
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:  
 63//Hs.113272:U90653  
 F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942  
 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830  
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.  
 14934:AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:  
 55 AB018268  
 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330  
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302  
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169  
 F-NT2RP3003552  
 F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322  
 F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365  
 5 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311  
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247  
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741  
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:  
 D14012  
 10 F-NT2RP3003625  
 F-NT2RP3003656  
 F-NT2RP3003659  
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586  
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184  
 15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:  
 63//Hs.44585:U58334  
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000  
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848  
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865  
 20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:  
 AB018300  
 F-NT2RP3003746  
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230  
 F-NT2RP3003799  
 25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:  
 M19722  
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:  
 242:57//Hs.114001:Z20656  
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//  
 30 5.1e-07:624:59//Hs.96028:AF042832  
 F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.  
 102877:U41315  
 F-NT2RP3003825  
 F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481  
 35 F-NT2RP3003831  
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:  
 AF070611  
 F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780  
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268  
 40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:  
 AB018343  
 F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]/6.8e-39:243:90//Hs.124832:AA846576  
 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]/1.1e-107:499:99//Hs.105794:AA701659  
 45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:  
 404:77//Hs.9006:AF057358  
 F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396  
 F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006  
 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.  
 50 93909:AF042498  
 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]/2.8e-127:617:97//Hs.  
 142151:AA984061  
 F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.  
 155302:U57317  
 55 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234  
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317  
 F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875  
 F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

100007:X76091  
 F-NT2RP3004093  
 F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258  
 F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390  
 5 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509  
 F-NT2RP3004145  
 F-NT2RP3004148  
 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:  
 10 AF032900  
 F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706  
 F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640  
 F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:  
 62//Hs.101047:M31523  
 15 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835  
 F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361  
 F-NT2RP3004242  
 F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240  
 F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140  
 20 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067  
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.  
 158471:AF088982  
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871  
 F-NT2RP3004332  
 25 F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285  
 F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426  
 F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999  
 F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
 III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915  
 30 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//  
 4.3e-125:608:98//Hs.128781:AA160707  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:  
 X97249  
 F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113  
 35 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403  
 F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:  
 AB007917  
 F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564  
 40 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219  
 F-NT2RP3004472  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925  
 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//  
 4.6e-118:547:99//Hs.124768:AA307735  
 45 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851  
 F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718  
 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256  
 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948  
 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046  
 50 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110  
 F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:  
 AB014532  
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:  
 55 AB011126  
 F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.  
 125870:AI364967  
 F-NT2RP3004569

- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923
- 5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
- F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336
- F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
- F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
- 10 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
- F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919
- F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
- F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
- 15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
- F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449
- 20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
- F-NT2RP4000111
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
- F-NT2RP4000150
- F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
- F-NT2RP4000159
- F-NT2RP4000167
- 30 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600
- F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
- F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
- 35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984
- F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470
- F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
- 40 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092
- F-NT2RP4000263
- F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
- 45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
- F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732
- F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
- F-NT2RP4000355
- 50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281
- F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
- F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
- 55 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678
- F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

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F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368  
F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688  
F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156  
5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984  
F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087  
F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468  
F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853  
10 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499  
F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535  
F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742  
F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995  
15 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293  
F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594  
F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904  
F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840  
20 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372  
F-NT2RP4000524  
F-NT2RP4000528  
F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154  
25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026  
F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351  
F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053  
F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730  
30 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513  
F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396  
F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907  
35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848  
F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783  
F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622  
40 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178  
F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440  
F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058  
F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162  
F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123  
45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939  
F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189  
F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833  
F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603  
50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278  
F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367  
F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803  
F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843  
55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142  
F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901  
F-NT2RP4000918  
F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

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F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503  
F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//  
Hs.24812:AF069532  
F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371  
5 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542  
F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888  
F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058  
F-NT2RP4000979  
F-NT2RP4000984  
10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U09013  
F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068  
F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204  
F-NT2RP4001004  
F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718  
15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.  
113287:AF009204  
F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494  
F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:  
L40157  
20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157  
F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:  
AJ006470  
F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497  
F-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.4e-131:634:98//Hs.  
25 106778:AJ010953  
F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.  
146459:X66975  
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164  
F-NT2RP4001095  
30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054  
F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
familiaris]//2.2e-26:171:92//Hs.14038:R06800  
F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142  
F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:  
35 100//Hs.126925:AA931237  
F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266  
F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261  
F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207  
F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171  
40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734  
F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324  
F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264  
F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324  
F-NT2RP4001207  
45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636  
F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251  
F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262  
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.  
122967:AF059569  
50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778  
F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463  
F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//  
Hs.31121:U40571  
F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578  
55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736  
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250  
F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110  
 F-NT2RP4001339  
 F-NT2RP4001343  
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39;686:64//Hs.112125:M12625  
 5 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds//2.0e-31:784:62//Hs.15432:U53445  
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356  
 F-NT2RP4001372  
 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194  
 10 F-NT2RP4001375  
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190  
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918  
 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957  
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:  
 AB018326  
 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.  
 20 26676:AA033997  
 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523  
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.  
 63220:AA522707  
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395  
 25 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260  
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863  
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494  
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:  
 U13220  
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534  
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174  
 F-NT2RP4001567  
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836  
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410  
 F-NT2RP4001574  
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228  
 F-NT2RP4001592  
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903  
 40 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952  
 F-NT2RP4001634  
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC  
 REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436  
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409  
 45 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECUR-  
 SOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629  
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:  
 67//Hs.30250:AF055376  
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080  
 50 F-NT2RP4001696  
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927  
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.  
 92614:M62302  
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198  
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878  
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656  
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:  
 AC004522



F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069  
 F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131  
 5 F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690  
 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888  
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:  
 10 AB014572  
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170  
 F-NT2RP4001889  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014  
 15 F-NT2RP4001896  
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848  
 F-NT2RP4001927  
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442  
 20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894  
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063  
 F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868  
 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:  
 25 788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047  
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560  
 30 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139  
 F-NT2RP4002052  
 F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873  
 F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999  
 35 F-NT2RP4002075  
 F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104  
 F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654  
 F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684  
 40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284  
 F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204  
 F-NT2RP4002888  
 F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960  
 F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995  
 45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071  
 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067  
 F-NT2RP5003492  
 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179  
 50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131  
 F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542  
 F-NT2RP5003522  
 F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943  
 55 F-NT2RP5003534  
 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934  
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

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F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:AI051983  
F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304  
F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922  
5 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060  
F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603  
F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549  
F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:H50008  
10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798  
F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543  
F-OVARC1000085  
F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442  
F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778  
15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600  
F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174  
F-OVARC1000109  
F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250  
20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134  
F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010  
F-OVARC1000139  
F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293  
25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414  
F-OVARC1000151  
F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305  
F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136  
30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131  
F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840  
F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834  
F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379  
35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984  
F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868  
F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306  
F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287  
F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI378579  
40 F-OVARC1000321  
F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946  
F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444  
45 F-OVARC1000347  
F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450  
F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930  
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162  
50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682  
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930  
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082  
F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615  
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416  
55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284  
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423  
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:AB014583

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F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524  
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640  
 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854  
 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926  
 5 F-OVARC1000479  
 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036  
 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850  
 F-OVARC1000526//ESTs//2.9e-08:368:611//Hs.42771:N26740  
 10 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492  
 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475  
 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667  
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410  
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:  
 15 66//Hs.85302:U76421  
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358  
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200  
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729  
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725  
 20 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722  
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881  
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
 plete cds//1.6e-78:424:93//Hs.86859:D43772  
 25 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:  
 AB011162  
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106  
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279  
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639  
 30 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.  
 125315:AF027156  
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306  
 F-OVARC 1000700  
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320  
 35 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//  
 1.2e-110:451:91//Hs.13476:AF038661  
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:  
 AI141736  
 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411  
 40 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196  
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//  
 Hs.157059:W28130  
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793  
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835  
 45 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584  
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032  
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:  
 AB014543  
 50 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584  
 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155  
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.  
 159234:U89995  
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143  
 55 F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323  
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777  
 F-OVARC 1000890  
 F-OVARC1000891

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F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818  
 F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691  
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456  
 5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440: M11119  
 F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078  
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs. 136243:AA307843  
 10 F-OVARC 1000948  
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986  
 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952  
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288  
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069  
 15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661  
 F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs. 155302:U57317  
 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458: AF088219  
 20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114  
 F-OVARC1001004  
 F-OVARC1001010  
 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866  
 F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076: 624:57//Hs.75063:AL023584  
 25 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149  
 F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074  
 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385  
 30 F-OVARC1001051  
 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs. 154968:U02020  
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873  
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451  
 35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs. 3426:AF082657  
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013  
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937  
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248  
 40 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584: AF051782  
 45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102  
 F-OVARC1001118  
 F-OVARC1001129  
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008  
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725  
 50 F-OVARC1001162  
 F-OVARC1001167  
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279  
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287  
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159  
 55 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapi- ens]//1.8e-11:192:69//Hs.130020:AA887581  
 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551  
 F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

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F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675

F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

5 F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837

10 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835

15 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.152455:AF044209

F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

20 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054

F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493

F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251

25 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715

F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633

F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777

F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554

30 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819

35 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242

F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426

40 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651

F-OVARC1001436

F-OVARC1001442

F-OVARC1001453

45 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823

F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568

F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507

50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243

F-OVARC1001525

F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

55 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299

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F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398  
 F-OVARC1001611  
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500  
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144  
 5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:  
 AB006867  
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229  
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858  
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807  
 10 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863  
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825  
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588  
 F-OVARC1001762  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 15 1.4e-150:706:98//Hs.155377:U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:  
 AB014575  
 F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697  
 F-OVARC1001791  
 20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830  
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102  
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:  
 AB018287  
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.  
 25 69949:M94172  
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825  
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453  
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567  
 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537  
 30 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973  
 F-OVARC1001861  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:  
 AF070611  
 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-  
 35 unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709  
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127  
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.  
 158095:AB007953  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 40 2.6e-57:300:96//Hs.6216:AF061749  
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834  
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261  
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263  
 F-OVARC1001928  
 45 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204  
 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III  
 [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794  
 F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251  
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228  
 50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639  
 F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:  
 213:78//Hs.105292:AA504776  
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:  
 55 AB007934  
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865  
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063  
 F-OVARC1002107

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F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174

F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913

F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022

5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795

F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097

F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868

F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568

10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517

F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230

F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928

F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789

15 F-PLACE1000014

F-PLACE1000031

F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088

F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494

F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755

20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499

F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771

F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366

25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082

F-PLACE1000094

F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378

F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135

30 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291

F-PLACE1000185

F-PLACE1000213

35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255

F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226

F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022

F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202

F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294

40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047

F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675

F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197

F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153

45 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024

F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516

F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260

50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174

F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053

F-PLACE1000424

F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590

55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) //2.7e-52:421:80//Hs.69747:M35531

F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638

F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

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F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353  
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573  
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289  
 5 F-PLACE1000562  
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538  
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179  
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542  
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:  
 10 AJ012449  
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751  
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542  
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986  
 F-PLACE1000636  
 15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265  
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896  
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:  
 20 69//Hs.128763:AF009353  
 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949  
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447  
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288  
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694  
 25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
 F-PLACE1000769  
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548  
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215  
 30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079  
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180  
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736  
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
 35 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428  
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
 F-PLACE1000948  
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821  
 40 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789  
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267  
 45 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432  
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633  
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876  
 50 F-PLACE1001024  
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741  
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204  
 F-PLACE1001062  
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859  
 55 F-PLACE1001088  
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485  
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:



71//Hs.150406:AF022158  
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704  
 F-PLACE1001168  
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135  
 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741  
 F-PLACE1001238  
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494  
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929  
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476  
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283  
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:  
 58//Hs.124161:AF065164  
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.  
 16533:D87930  
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052  
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385  
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342  
 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:  
 AF009615  
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748  
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:  
 117:84//Hs.21301:AF093419  
 25 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE  
 EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646  
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete  
 CDS//0.0038:496:57//Hs.97681:AJ223333  
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.  
 30 154069:U06452  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:  
 AF091087  
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232  
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987  
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510  
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455  
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716  
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529  
 F-PLACE1001503  
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914  
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753  
 F-PLACE1001545  
 F-PLACE1001551  
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835  
 45 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233  
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987  
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230  
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005  
 F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690  
 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:  
 AB018341  
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198  
 F-PLACE1001640  
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927  
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-  
 148:726:96//Hs.3688:AF069250  
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN  
 [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

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F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776

F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686

5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094

F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052

F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159

F-PLACE1001745

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243

F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283

F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050

15 F-PLACE1001781

F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115

F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953

20 F-PLACE1001821

F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494

F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214

F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906

25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257

F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220

F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936

F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837

30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778

F-PLACE1001989

F-PLACE1002004

F-PLACE1002046

F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108

35 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555

F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178

F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765

40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637

F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831

F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747

F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631

45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390

F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891

F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627

F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674

F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289

50 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989

F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675

55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291

F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710

F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

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F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148  
F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947  
5 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158  
F-PLACE1002465  
F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581  
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523  
F-PLACE1002493  
10 F-PLACE1002499  
F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010  
F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482  
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:  
15 AB018256  
F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774  
F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369  
F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866  
20 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627  
F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725  
F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497  
F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187  
25 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915  
F-PLACE1002625  
F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412  
F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706  
F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:  
30 804:97//Hs.124903:AF068180  
F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903  
F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971  
F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080  
35 F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728  
F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827  
F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516  
F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926  
40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994  
F-PLACE1002815  
F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691  
F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163  
F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167  
45 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405  
F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024  
F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627  
F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029  
F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056  
50 F-PLACE1002962  
F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815  
F-PLACE1002991  
F-PLACE1002993  
F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959  
55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979  
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088

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F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567  
F-PLACE1003045  
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491  
5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875  
F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419  
F-PLACE1003136  
F-PLACE1003145  
F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590  
10 F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997  
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797  
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209  
F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532  
15 F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770  
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208  
F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:X57025  
F-PLACE1003256  
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802  
20 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106  
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376  
F-PLACE1003334  
F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308  
25 F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568  
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715  
F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277  
30 F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575  
F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858  
F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009  
F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069  
F-PLACE1003383  
35 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546  
F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178  
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846  
F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912  
40 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874  
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635  
F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627  
F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145  
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633  
45 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248  
F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428  
F-PLACE1003553  
F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780  
F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367  
50 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932  
F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194  
F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620  
F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965  
55 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961  
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200  
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104

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F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896  
F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503  
F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105  
F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762  
5 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413  
F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299  
F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305  
F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101  
10 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553  
F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344  
F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648  
15 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983  
F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629  
F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944  
F-PLACE1003783  
F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308  
20 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169  
F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786  
F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165  
F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124  
F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359  
25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257  
F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770  
F-PLACE1003886  
F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108  
F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050  
30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944  
F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142  
F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069  
F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585  
35 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537  
F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536  
F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412  
F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812  
40 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940  
F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516  
F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.153045:X52056  
F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526  
45 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779  
F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552  
F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785  
F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666  
50 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201  
F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493  
F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722  
F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273  
55 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689  
F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128  
F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

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F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914

F-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830

5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884

F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588

F-PLACE1004336

10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108

F-PLACE1004388

15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283

20 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867

F-PLACE1004460

F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363

F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085

F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416

25 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163

F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680

F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445

F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150

30 F-PLACE1004518

F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314

F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854

F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371

35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299

F-PLACE1004645

F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991

F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590

F-PLACE1004664

40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606

F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589

45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561

F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131

F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542

F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891

50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148

F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680

F-PLACE1004743

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470

55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367

F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391

F-PLACE1004793

F-PLACE1004804

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F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340  
 F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]/2.4e-78:415:95//Hs.80965:AA493284  
 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362  
 5 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047  
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943  
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669  
 F-PLACE1004838  
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910  
 10 F-PLACE1004868  
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772  
 F-PLACE1004900  
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382  
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929  
 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130  
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936  
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592  
 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851  
 F-PLACE1004969  
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605  
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147  
 25 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520  
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831  
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459  
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159  
 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943  
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569  
 35 F-PLACE1005077//EST//0.79:283:591//Hs.89276:AA283899  
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740  
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147  
 40 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401  
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561  
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366  
 F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227  
 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661  
 F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]/4.8e-12:360:63//Hs.142177:H11741  
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087  
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541  
 50 F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]/4.4e-126:583:99//Hs.25347:AI138605  
 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417  
 F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009  
 55 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]/0.56:192:60//Hs.47334:W72370  
 F-PLACE1005243  
 F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

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F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182  
 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947  
 5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673  
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534  
 F-PLACE1005313  
 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650  
 10 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794  
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297  
 F-PLACE1005373  
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348  
 15 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751  
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951  
 F-PLACE1005467//HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433  
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925  
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503  
 20 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323  
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973  
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029  
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105  
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747  
 25 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572  
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335  
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385  
 F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144  
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261  
 30 F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278  
 F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436  
 F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594  
 F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851  
 35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057  
 F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234  
 F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867  
 F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991  
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255  
 40 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618  
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917  
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457  
 45 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437  
 F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944  
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258  
 F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302  
 50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696  
 F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493  
 F-PLACE1005802  
 F-PLACE1005803  
 55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156  
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482



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F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986  
F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870  
F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497  
5 F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905  
F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242  
F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487  
F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552  
F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300  
10 F-PLACE1005898  
F-PLACE1005921  
F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504  
F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274  
F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:  
15 M18391  
F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142  
F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978  
F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357  
F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468  
20 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868  
F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:  
U13948  
F-PLACE1005968  
F-PLACE1005990  
25 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981  
F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256  
F-PLACE1006011  
F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743  
F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:  
30 AB018332  
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906  
F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395  
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:  
AF039023  
35 F-PLACE1006129  
F-PLACE1006139  
F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353  
F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:  
R92857  
40 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868  
F-PLACE10061641//ESTs//0.099:223:60//Hs.8108:AA902721  
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239  
F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005  
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433  
45 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608  
F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.  
135623:AA134719  
F-PLACE1006205  
F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]  
50 //0.0089:166:63//Hs.127179:AI279486  
F-PLACE1006225  
F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668  
F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185  
F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802  
55 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:  
AB014548  
F-PLACE1006262  
F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

F-PLACE1006318  
 F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503  
 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492  
 F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249  
 5 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481  
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581  
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715  
 F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693  
 10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085  
 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296  
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735  
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129  
 15 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866  
 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381  
 F-PLACE1006470  
 20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194  
 F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511  
 F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493  
 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584  
 25 F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542  
 F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358  
 F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219  
 F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784  
 30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529  
 F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280  
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670  
 35 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088  
 F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858  
 F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396  
 F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473  
 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917  
 40 F-PLACE1006678  
 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403  
 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612  
 F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354  
 45 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152  
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252  
 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783  
 F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228  
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941  
 50 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017  
 F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892  
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518  
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503  
 55 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876  
 F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773  
 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273  
 F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

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F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601  
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187  
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443  
 F-PLACE1006917  
 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913  
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211  
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565  
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723  
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.  
 10 21806:AA630312  
 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417  
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:  
 191:67//Hs.8813:AF032922  
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753  
 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//  
 3.1e-05:594:58//Hs.32951:AF034102  
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971  
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503  
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957  
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243  
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987  
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type III)//0.18:268:63//Hs.904:U84010  
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385  
 25 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669  
 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//  
 Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:  
 L06133  
 F-PLACE1007282  
 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412  
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//  
 Hs.144877:AF029403  
 F-PLACE1007342  
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:  
 567:98//Hs.76596:AF096870  
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173  
 F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642  
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287  
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//  
 Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436  
 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391  
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714  
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

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F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975  
 F-PLACE1007488  
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385  
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503  
 5 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296  
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979  
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080  
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755  
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:  
 10 AB014561  
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863  
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257  
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163  
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533  
 15 F-PLACE1007621  
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867  
 F-PLACE1007645  
 F-PLACE1007649  
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266  
 20 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055  
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503  
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812  
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953  
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:  
 25 AF061243  
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:  
 AA476815  
 F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:  
 64//Hs.104129:AA923278  
 30 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:  
 AB014585  
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424  
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030  
 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469  
 35 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656  
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504  
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107  
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841  
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635  
 40 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503  
 F-PLACE1007852  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:  
 AB018309  
 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387  
 45 F-PLACE1007877  
 F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.  
 92381:AB007956  
 F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002  
 50 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.  
 5671:AF084530  
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:  
 730:98//Hs.78106:AF079529  
 55 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:  
 W28567  
 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043  
 F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

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F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031  
 F-PLACE1008044  
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382  
 5 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060  
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975  
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197  
 10 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769  
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874  
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683  
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]/5.1e-20:124:95//Hs.146238:AI263135  
 15 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427  
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524  
 F-PLACE1008201  
 F-PLACE1008209  
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856  
 20 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385  
 F-PLACE1008273  
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113  
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970  
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287  
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071  
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129  
 30 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]/5.4e-74:356:98//Hs.105382:AA496362  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579  
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569  
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911  
 35 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171  
 F-PLACE1008398  
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326  
 40 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943  
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653  
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499  
 45 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]/0.019:530:58//Hs.72248:S72487  
 F-PLACE1008437  
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335  
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901  
 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381  
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886  
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823  
 55 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697  
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081  
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997  
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

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F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334  
 5 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326  
 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794  
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560  
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458  
 F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211  
 10 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394  
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535  
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333  
 F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728  
 15 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406  
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741  
 F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080  
 20 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503  
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543  
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772  
 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542  
 25 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905  
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883  
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858  
 30 F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728  
 F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563  
 F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503  
 F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323  
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308  
 35 F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771  
 F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026  
 F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937  
 F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308  
 40 F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950  
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112  
 F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762  
 F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689  
 45 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585  
 F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698  
 F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525  
 F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800  
 50 F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091  
 F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031  
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011  
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890  
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788  
 55 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586  
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215  
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108

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F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953

F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302

5 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250

F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821

F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100

10 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396

F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689

F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131

F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540

F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575

15 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735

F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192

20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630

30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872

F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678

35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A//4.1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

40 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291.

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

45 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

50 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

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F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789  
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024  
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989  
 5 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-  
 130:600:95//Hs.16411:AL030996  
 F-PLACE1009845  
 10 F-PLACE1009861  
 F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021  
 F-PLACE1009886  
 F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889  
 F-PLACE1009908  
 15 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717  
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379  
 F-PLACE1009925  
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153  
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446  
 20 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345  
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114  
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540  
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:  
 AB014529  
 25 F-PLACE1010023  
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878  
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.  
 142151:AA984061  
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596  
 30 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:  
 AF065482  
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424  
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925  
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus  
 musculus]//1.8e-38:212:95//Hs.98067:AA236822  
 35 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:  
 U69567  
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:  
 AF020761  
 40 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.  
 122967:AF059569  
 F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682  
 F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889  
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740  
 45 F-PLACE1010152  
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792  
 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582  
 F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:  
 H69637  
 50 F-PLACE1010231  
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:  
 AB007917  
 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590  
 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540  
 55 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813  
 F-PLACE1010310//HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433  
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248  
 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875



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F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659  
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117  
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855  
 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648  
 5 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986  
 F-PLACE1010401  
 F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824  
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:  
 AF039081  
 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500  
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100  
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:  
 64//Hs.159273:AF054177  
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472  
 15 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979  
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148  
 F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06  
 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661  
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete  
 20 cds//9.9e-148:707:97//Hs.19851:AF045186  
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394  
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858  
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778  
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200  
 25 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461  
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225  
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102  
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076  
 F-PLACE1010662  
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.  
 37138:U35376  
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027  
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:  
 96//Hs.50758:AF092564  
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:  
 AJ131244  
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391  
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus lae-  
 vis]//5.1e-80:407:96//Hs.80965:AA493284  
 40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //6.0e-45:251:94//Hs.11379:AA594140  
 F-PLACE1010786  
 F-PLACE1010800  
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157  
 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085  
 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.  
 132736:AA583494  
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048  
 F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.  
 50 130135:AA905493  
 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:  
 AB011182  
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671  
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169  
 F-PLACE1010900  
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981  
 F-PLACE1010917

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F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537  
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126  
5 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:AF064244  
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985  
F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154  
F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506  
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632  
10 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721  
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931  
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032  
F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886  
15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678  
F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194  
F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//Hs.153640:U56998  
20 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320  
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663  
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037  
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317  
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857  
25 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949  
F-PLACE1011160  
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443  
F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114  
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664  
30 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]/9.7e-101:469:99//Hs.8241:AA283057  
F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]/2.6e-62:221:88//Hs.101821:W27452  
F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751  
35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:AB011101  
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014  
F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803  
F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:AF070637  
40 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915  
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160  
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310  
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265  
45 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970  
F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535  
F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]/6.7e-68:325:99//Hs.107245:AA627053  
50 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868  
F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552  
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102  
55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503  
F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204  
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255

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F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482  
F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264  
F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997  
5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319  
F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476  
F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333  
F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180  
10 F-PLACE1011586//Homo sapiens hLRpl05 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462  
F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778  
F-PLACE1011641  
F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631  
15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661  
F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086  
F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745  
F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640  
F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234  
20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366  
F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350  
F-PLACE1011725  
F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853  
F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891  
25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240  
F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693  
F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660  
F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664  
F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775  
30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152  
F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913  
F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868  
F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817  
F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617  
35 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763  
F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514  
F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591  
F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514  
40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256  
F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956  
F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503  
45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330  
F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627  
F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831  
F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627  
F-PLACE2000017  
50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557  
F-PLACE2000030  
F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512  
F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179  
55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204  
F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128  
F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966  
F-PLACE2000061

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F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457  
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:  
 AF027219  
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333  
 5 F-PLACE2000100  
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219  
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:  
 U56417  
 F-PLACE2000115  
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353  
 F-PLACE2000132  
 F-PLACE2000136//ESTS, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:  
 AA718911  
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645  
 15 F-PLACE2000164  
 F-PLACE2000170  
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179  
 F-PLACE2000176  
 F-PLACE2000187  
 20 F-PLACE2000216  
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933  
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296  
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338  
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:  
 25 AB007958  
 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522  
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560  
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869  
 F-PLACE2000317  
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:  
 M89796  
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088  
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299  
 F-PLACE2000347//ESTs, Moderately similar to F18547\_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817  
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645  
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045  
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861  
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032  
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638  
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.  
 158095:AB007953  
 F-PLACE2000398  
 F-PLACE2000399  
 F-PLACE2000404  
 45 F-PLACE2000411  
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-  
 20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-  
 55 05:100:73//Hs.104239:AA488082  
 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241  
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

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F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,  
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384  
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128  
 F-PLACE3000029  
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248  
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842  
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.  
 122752:AF026445  
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295  
 10 F-PLACE3000121  
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081  
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603  
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243  
 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016  
 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871  
 F-PLACE3000148  
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:  
 AB014572  
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023  
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:  
 U79666  
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:  
 AB011147  
 F-PLACE3000160  
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219  
 F-PLACE3000194  
 F-PLACE3000197  
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546  
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975  
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//  
 Hs.77522:X62744  
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216  
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377  
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-  
 35 56:200:85//Hs.133089:AF064019  
 F-PLACE3000226  
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568  
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
 40 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
 nomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046  
 F-PLACE3000244  
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858  
 F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650  
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944  
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770  
 F-PLACE3000310  
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586  
 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219  
 50 F-PLACE3000331  
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:  
 AB014545  
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741  
 F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis ele-  
 55 gans]//2.9e-59:474:77//Hs.125850:AA885355  
 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194  
 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:  
 234:63//Hs.7498:U41514

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F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441  
 F-PLACE3000363  
 F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928  
 F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641  
 5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432  
 F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637  
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785  
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270  
 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715  
 10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541  
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:  
 116:78//Hs.77579:AF013263  
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:  
 H61502  
 15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:  
 AB018344  
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161  
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:  
 183:93//Hs.108326:AB006202  
 20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874  
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888  
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:  
 AB018352  
 25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:  
 AC004131  
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533  
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.  
 40993:AF000148  
 30 F-PLACE4000063  
 F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713  
 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819  
 F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058  
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:  
 35 AB007931  
 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751  
 F-PLACE4000129  
 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627  
 F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856  
 40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367  
 F-PLACE4000192  
 F-PLACE4000211  
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594  
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329  
 45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317  
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250  
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609  
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886  
 50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200  
 F-PLACE4000261  
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:  
 100//Hs.118849:AA215645  
 F-PLACE4000270  
 55 F-PLACE4000300  
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966  
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365  
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

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F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292  
 F-PLACE4000367  
 F-PLACE4000369  
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256  
 5 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823  
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:  
 AB014540  
 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982  
 10 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200  
 F-PLACE4000445  
 F-PLACE4000450  
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874  
 F-PLACE4000487//Sialoporphin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075  
 15 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951  
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289  
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731  
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECUR-  
 SOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022  
 20 F-PLACE4000548  
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:  
 AF000986  
 F-PLACE4000581  
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-  
 13:275:68//Hs.113980:AI034080  
 25 F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675  
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074  
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:  
 AB002446  
 30 F-PLACE4000650  
 F-PLACE4000654  
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132  
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299  
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila  
 melanogaster]//2.5e-36:197:96//Hs.118634:U66688  
 35 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:  
 AB014554  
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254  
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877  
 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194  
 F-THYRO1000034  
 F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099  
 F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326  
 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345  
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557  
 F-THYRO1000085  
 F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065  
 F-THYRO1000107  
 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503  
 F-THYRO1000121  
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732  
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:  
 AF087142  
 55 F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203  
 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416  
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219  
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

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152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590

F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520

35 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

45 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380



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F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324  
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204  
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871  
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:  
 AF061573  
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481  
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:  
 10 452:58//Hs.11538:AF006084  
 F-THYRO1000787  
 F-THYRO1000793  
 F-THYRO1000796  
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:  
 15 AB002446  
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087  
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339  
 F-THYRO1000843  
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788  
 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170  
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:  
 20 190:75//Hs.133526:N21103  
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531  
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.  
 25 92381:AB007956  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:  
 839:98//Hs.78106:AF079529  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836  
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263  
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963  
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear  
 gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169  
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907  
 F-THYRO1000983  
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646  
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307  
 F-THYRO1001003  
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369  
 F-THYRO1001033//H.sapiens mRNA for cyclicin II//0.0061:287:60//Hs.3232:Z46788  
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830  
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130  
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700  
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416  
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425  
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074  
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788  
 F-THYRO1001173  
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385  
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163  
 F-THYRO1001204  
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219  
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461  
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309  
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:  
 AF027156  
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836  
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

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F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872  
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333  
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545  
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207  
 5 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939  
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607  
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993  
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946  
 F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694  
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659  
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788  
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//  
 15 Hs.102877:U41315  
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099  
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215  
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830  
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943  
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904  
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663  
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211  
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046  
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335  
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572  
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655  
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535  
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849  
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071  
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046  
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659  
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463  
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568  
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089  
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238  
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552  
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691  
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560  
 F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229  
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813  
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590  
 45 F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725  
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324  
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295  
 F-THYRO1001828  
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823  
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:M24283  
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198  
 F-VESEN1000122  
 55 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885  
 F-Y79AA1000033  
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

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U78521  
F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680  
F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053  
5 F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt//  
0.0022:684:58//Hs.83190:U29344  
F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860  
F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.  
9242:AF081192  
F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079  
10 F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623  
F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134  
F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365  
F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919  
F-Y79AA1000328  
15 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:  
AF071309  
F-Y79AA1000346  
F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853  
F-Y79AA1000355  
20 F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908  
F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897  
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219  
F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018  
F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:  
25 AF082516  
F-Y79AA1000480  
F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871  
F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521  
F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356  
30 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:  
AF068706  
F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716  
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:  
AF091080  
35 F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:  
AF060503  
F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513  
F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:  
98//Hs.83023:AF093670  
40 F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969  
F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377  
F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067  
F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468  
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:  
45 AF098799  
F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231  
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085  
F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:  
AF059569  
50 F-Y79AA1000805  
F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568  
F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt//  
0.0048:630:57//Hs.83190:U29344  
F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956  
55 F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644  
F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:  
D16815  
F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]/6.9e-69:310:94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
- F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
- 10 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
- F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
- 15 F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
- F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
- F-Y79AA1001177//Human hSLAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
- F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
- F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
- F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
- F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
- F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
- F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
- F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependept kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
- F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
- 45 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
- F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
- F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
- F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
- 55 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
- F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
- F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

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F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533  
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124  
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332  
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778  
 5 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173  
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720  
 F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382  
 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611  
 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943  
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045  
 F-Y79AA1002093  
 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865  
 F-Y79AA1002115  
 15 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395  
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955  
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538  
 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515  
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:  
 20 96//Hs.111637:AA305890  
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984  
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477  
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045  
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:  
 AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:  
 AB014555  
 30 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:  
 AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 35 cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 40 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302  
 45

## Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

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R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434  
R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233  
R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198  
5 R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087  
R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340  
R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329  
R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788  
R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.  
10 55918:AA151667  
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340  
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540  
15 R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237  
R-HEMBA1000158  
R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863  
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545  
20 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366  
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927  
R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847  
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311  
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532  
25 R-nnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404  
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874  
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944  
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019  
30 R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808  
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424  
R-nnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920  
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485  
35 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962  
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409  
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099  
R-nnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323  
R-nnnnnnnnnnnn//Human Ca2+-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//  
40 Hs.151301:U36448  
R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024  
R-nnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238  
R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560  
R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//  
45 Hs.73614:U83460  
R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243  
R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629  
R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857  
50 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938  
R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960  
R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//  
Hs.73614:U83460  
R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878  
55 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248  
R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920  
R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282

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R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700  
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140  
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189  
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143  
 5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014  
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349  
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316  
 R-HEMBA1000460  
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370  
 10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219  
 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449  
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528  
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087  
 15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571  
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318  
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531  
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885  
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414  
 20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280  
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782  
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277  
 25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809  
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317  
 R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699  
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881  
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481  
 30 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196  
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788  
 35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944  
 R-HEMBA1000591//Homo sapiens mRNA for ElB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509  
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE  
 ITK/TSK//0.024:309:61//Hs.89519:L10717  
 40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041  
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136  
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424  
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438  
 45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235  
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590  
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390  
 50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929  
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136  
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922  
 R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736  
 55 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280  
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

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R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213  
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612  
5 R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931  
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777  
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110  
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219  
10 R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131  
R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219  
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612  
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795  
15 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087  
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939  
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027  
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977  
20 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258  
R-HEMBA1000851  
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689  
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794  
25 R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202  
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608  
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951  
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219  
R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154  
30 R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672  
R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508  
R-HEMBA1000919  
R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597  
R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619  
35 R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291  
R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074  
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750  
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977  
40 R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498  
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590  
R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170  
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878  
45 R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464  
R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902  
R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881  
R-HEMBA1001007  
R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764  
50 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836  
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937  
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360  
55 R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292  
R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912  
R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336  
R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543



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R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616  
R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521  
5 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886  
R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813  
R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420  
R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961  
R-HEMBA1001080  
10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788  
R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674  
R-HEMBA1001094  
R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245  
R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219  
15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974  
R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320  
R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530  
R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341  
R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265  
20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219  
R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358  
R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961  
25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896  
R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194  
R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080  
R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316  
30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932  
R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728  
R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181  
R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674  
35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534  
R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324  
R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219  
R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162  
R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214  
40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019  
R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977  
R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950  
R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838  
45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259  
R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080  
R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816  
R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837  
R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334  
50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550  
R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458  
R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482  
R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439  
R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204  
55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081  
R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714  
R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364  
R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

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R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199  
 R-HEMBA1001415  
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981  
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704  
 5 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263  
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982  
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546  
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077  
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503  
 10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220  
 R-HEMBA1001463  
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008  
 R-HEMBA1001478  
 R-HEMBA1001497  
 15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426  
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503  
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269  
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493  
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723  
 20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270  
 R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348  
 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219  
 R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324  
 R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880  
 25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030  
 R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652  
 R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329  
 R-HEMBA1001589  
 R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874  
 30 R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627  
 R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530  
 R-nnnnnnnnnnnnn/Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694  
 35 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158  
 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623  
 R-nnnnnnnnnnnnn/ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398  
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554  
 R-HEMBA1001658  
 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343  
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943  
 R-HEMBA1001675  
 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598  
 50 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
 R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452  
 55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219  
 R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105  
 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

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R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353  
R-HEMBA1001744  
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
R-nnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019  
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969  
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334  
15 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179  
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290  
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210  
20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250  
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517  
25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:Z48051  
R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329  
30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969  
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128  
R-HEMBA1001910  
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438  
35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685  
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145  
40 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470  
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390  
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825  
50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178  
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
55 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353  
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801  
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

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R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550  
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
 R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312  
 5 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135  
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369  
 10 R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402  
 R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854  
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868  
 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957  
 15 R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734  
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199  
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642  
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337  
 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674  
 20 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915  
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043  
 R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081  
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457  
 25 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622  
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958  
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357  
 30 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503  
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342  
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315  
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151  
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606  
 35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814  
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202  
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426  
 40 R-HEMBA1002257  
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675  
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314  
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595  
 45 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818  
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314  
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822  
 50 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094  
 R-nnnnnnnnnnnnn/Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563  
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435  
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237  
 55 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954  
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849  
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267  
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

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R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069  
 R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085  
 R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395  
 5 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394  
 R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219  
 R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995  
 R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133  
 R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449  
 10 R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990  
 R-HEMBA1002508//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:  
 AJ011972  
 R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:  
 15 AB007923  
 R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700  
 R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804  
 R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881  
 R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012  
 20 R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519  
 R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219  
 R-HEMBA1002561//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:  
 AF075587  
 R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904  
 25 R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838  
 R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:  
 AB018351  
 30 R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881  
 R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715  
 R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041  
 R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970  
 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-  
 35 plete cds//1.5e-53:406:81//Hs.108966:U48696  
 R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:  
 AB018307  
 R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945  
 R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-  
 40 104:560:92//Hs.161748:T64896  
 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282  
 R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477  
 R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:  
 45 AB018315  
 R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884  
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:  
 AB014521  
 R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168  
 50 R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163  
 R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526  
 R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792  
 R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090  
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:  
 55 AB011126  
 R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127  
 R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491  
 R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

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R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333  
 R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709  
 R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320  
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:  
 5 AF071185  
 R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204  
 R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013  
 R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.  
 5337:AA243757  
 10 R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514  
 R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830  
 R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827  
 R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670  
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//  
 15 Hs.33787:AF037261  
 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011  
 R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820  
 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087  
 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481  
 20 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165  
 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679  
 R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732  
 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892  
 R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085  
 25 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369  
 R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405  
 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579  
 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219  
 R-nnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064  
 30 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:  
 96//Hs.125749:AI377682  
 R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080  
 R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480  
 R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577  
 35 R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827  
 R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366  
 R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN  
 CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442  
 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-  
 40 119:578:97//Hs.44097:AF054182  
 R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627  
 R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238  
 R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903  
 R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235  
 45 R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402  
 R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249  
 R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223  
 R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//  
 50 Hs.104800:AA709155  
 R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624  
 R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058  
 R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.  
 118717:U86751  
 55 R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845  
 R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharo-  
 myces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615  
 R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

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R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670  
 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933  
 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389  
 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000  
 5 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804  
 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:  
 AB014540  
 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943  
 R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265  
 10 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR  
 [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817  
 R-HEMBA1003227//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:  
 W27666  
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305  
 15 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834  
 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.  
 152663:AF068864  
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929  
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219  
 20 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392  
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785  
 R-HEMBA1003281  
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:  
 AB011109  
 25 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266  
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353  
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504  
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.  
 124224:AB001872  
 30 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869  
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119  
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173  
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:  
 AF026029  
 35 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357  
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540  
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651  
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588  
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247  
 40 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-  
 11:261:65//Hs.87578:AI125363  
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847  
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127  
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204  
 45 R-HEMBA1003417//ESTs//1.7e-24:188:85//Hs.70266:Z78309  
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563  
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013  
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696  
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121  
 50 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516  
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080  
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688  
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760  
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058  
 55 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817  
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673  
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.  
 91619:AA552351

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R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734  
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522  
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058  
 5 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440  
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099  
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892  
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065  
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212  
 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087  
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042  
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374  
 R-HEMBA1003615  
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167  
 15 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387  
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888  
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021  
 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438  
 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830  
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010  
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783  
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957  
 25 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049  
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635  
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329  
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083  
 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379  
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916  
 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873  
 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064  
 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777  
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080  
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823  
 40 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847  
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839  
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592  
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040  
 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247  
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089  
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214  
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327  
 50 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600  
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236  
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868  
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295  
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344  
 55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163  
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333



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R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161  
 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033  
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547  
 5 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sa-  
 piens]//2.1e-59:295:98//Hs.161661:AA166911  
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621  
 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930  
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179  
 R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788  
 10 R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187  
 R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659  
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157  
 R-HEMBA1003939  
 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669  
 15 R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545  
 R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591  
 R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562  
 R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253  
 R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525  
 20 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882  
 R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:  
 448:97//Hs.117834:AA766771  
 R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756  
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682  
 25 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105  
 R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899  
 R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011  
 R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774  
 R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461  
 30 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191  
 R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253  
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804  
 R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469  
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717  
 35 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754  
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080  
 R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988  
 R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652  
 R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251  
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918  
 R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562  
 R-HEMBA1004133  
 R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736  
 R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320  
 45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219  
 R-HEMBA1004150//GRANCALCIN//0.99:357:59//Hs.79381:M81637  
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087  
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855  
 R-HEMBA1004199  
 50 R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701  
 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.  
 10092:AI189282  
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:  
 AB014518  
 55 R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748  
 R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617  
 R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-  
 16:117:91//Hs.92033:AA255832

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R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353  
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389  
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258  
5 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284  
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962  
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018  
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931  
10 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228  
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795  
15 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061  
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961  
20 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426  
R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679  
R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281  
R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904  
R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714  
25 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561  
R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231  
R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336  
R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240  
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:  
30 D89667  
R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353  
R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494  
R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869  
35 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057  
R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264  
R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084  
R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219  
R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717  
40 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933  
R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518  
R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503  
45 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829  
R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033  
R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172  
R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306  
R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034  
50 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941  
R-HEMBA1004507  
R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271  
R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947  
55 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972  
R-HEMBA1004554  
R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

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R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913  
 R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243  
 R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769  
 R-nnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661  
 5 R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970  
 R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915  
 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785  
 10 R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152  
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393  
 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454  
 R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442  
 15 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348  
 R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560  
 R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368  
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252  
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562  
 20 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042  
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881  
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219  
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235  
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317  
 25 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151  
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275  
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828  
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651  
 30 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428  
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081  
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498  
 R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679  
 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504  
 35 R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380  
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705  
 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092  
 R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633  
 40 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476  
 R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167  
 R-nnnnnnnnnnnn  
 R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732  
 R-HEMBA1004806  
 45 R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676  
 R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002  
 R-HEMBA1004847  
 50 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120  
 R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267  
 R-HEMBA1004864  
 R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362  
 R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409  
 55 R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676  
 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470  
 R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011  
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

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R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388  
R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053  
R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053  
5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883  
R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215  
R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434  
R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007  
R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074  
10 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040  
R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035  
R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065  
R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404  
R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683  
15 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329  
R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894  
R-HEMBA1004995  
R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520  
20 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212  
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548  
R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382  
25 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067  
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348  
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436  
R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145  
30 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451  
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905  
R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789  
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077  
R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958  
35 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561  
R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739  
R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952  
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173  
40 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957  
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694  
R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397  
45 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914  
R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766  
R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239  
R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836  
50 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284  
R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687  
R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331  
R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834  
R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896  
55 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157  
R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862  
R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391  
R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

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R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750  
 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219  
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519  
 R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046  
 5 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169  
 R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472  
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606  
 R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467  
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.  
 10 129735:AF010144  
 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350  
 R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653  
 R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305  
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150  
 15 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:  
 92//Hs.43864:AA131568  
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278  
 R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725  
 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059  
 20 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757  
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:  
 453:99//Hs.4854:AF041248  
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960  
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391  
 25 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961  
 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494  
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353  
 R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:  
 K00627  
 30 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445  
 R-HEMBA1005497  
 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788  
 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//  
 Hs.62608:S58544  
 35 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870  
 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:  
 AI219740  
 R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322  
 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045  
 40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981  
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788  
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.  
 17035:AI080471  
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350  
 45 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926  
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627  
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193  
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:  
 182:76//Hs.133526:N21103  
 50 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709  
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497  
 R-HEMBA1005577  
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538  
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392  
 55 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539  
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990  
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905  
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

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R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125  
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390  
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422  
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.  
 5 19400:AA662845  
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377  
 R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081  
 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522  
 R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.  
 10 10458:AF088219  
 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973  
 R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477  
 R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450  
 R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258  
 15 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:  
 U44060  
 R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//  
 1.7e-47:376:84//Hs.26988:U66406  
 R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055  
 20 R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943  
 R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:  
 AJ006470  
 R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815  
 R-nnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672  
 25 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096  
 R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:  
 U21936  
 R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974  
 R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.  
 30 10458:AF088219  
 R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601  
 R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960  
 R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201  
 R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618  
 35 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911  
 R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917  
 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970  
 R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252  
 R-HEMBA1005894  
 40 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686  
 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363  
 R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632  
 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:  
 AB011098  
 45 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867  
 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418  
 R-HEMBA1005963  
 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.  
 26285:AF082516  
 50 R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199  
 R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618  
 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875  
 R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436  
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268  
 55 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951  
 R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508  
 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490  
 R-nnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612  
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517  
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313  
 5 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//  
 Hs.73614:U83460  
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297  
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293  
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931  
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635  
 10 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906  
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125  
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557  
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//  
 20 Hs.23617:AA928683  
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522  
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:  
 AF083384  
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881  
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.  
 10552:AA524401  
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:  
 92//Hs.104129:AA923278  
 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.  
 30 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821  
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735  
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019  
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037  
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:  
 U33931  
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:  
 AI204587  
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219  
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184  
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204  
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075  
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382  
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008  
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787  
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830  
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:  
 AB011166  
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651  
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5 82:84//Hs.23094:M19503  
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923  
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778  
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878  
 55 R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004  
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964  
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380  
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

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R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784  
 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895  
 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]/3.0e-17:342:63//Hs.111730:AA604403  
 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441  
 5 R-HEMBA1006474  
 R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984  
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701  
 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223  
 10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350  
 R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720  
 R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387  
 R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117  
 R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505  
 15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566  
 R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300  
 R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628  
 R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934  
 20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331  
 R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154  
 R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]/1.8e-109:547:96//Hs.21122:AA191594  
 R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064  
 25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876  
 R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725  
 R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876  
 R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280  
 30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390  
 R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219  
 R-HEMBA1006612  
 R-nnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247  
 R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630  
 35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067  
 R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]/2.7e-91:426:100//Hs.139469:AI299889  
 R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]/3.4e-37:186:100//Hs.109818:AA411185  
 40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777  
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282  
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511  
 45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102  
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594  
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842  
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435  
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263  
 50 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695  
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]/1.1e-92:483:94//Hs.6525:AI205313  
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062  
 55 R-HEMBA1006717  
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002  
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627  
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099



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R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646  
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763  
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881  
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562  
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936  
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705  
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978  
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333  
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305  
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272  
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556  
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087  
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665  
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:  
 15 AB018315  
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453  
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739  
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117  
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400  
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308  
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712  
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382  
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:  
 AJ010841  
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321  
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457  
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827  
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325  
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679  
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440  
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293  
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363  
 R-HEMBA1007045  
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788  
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839  
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140  
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272  
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866  
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-  
 40 40:163:83//Hs.152369:AA504818  
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087  
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025  
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597  
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272  
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438  
 R-HEMBA1007147  
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818  
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674  
 R-nnnnnnnnnnnnn/Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085  
 50 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954  
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987  
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990  
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:  
 55 AB018340  
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864  
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934  
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

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R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062  
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207  
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543  
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804  
 5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990  
 R-HEMBA1007301  
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917  
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/5.5e-15:311:64//Hs.142764:AA205569  
 10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629  
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452  
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848  
 15 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684  
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333  
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]/3.3e-44:341:71//Hs.111730:AA604403  
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090  
 20 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969  
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418  
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332  
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449  
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]/6.0e-92:477:95//Hs.4877:AA418465  
 25 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928  
 R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702  
 R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954  
 30 R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802  
 R-HEMBA1000050//ESTs//0.039:91:74//Hs.163189:AA236903  
 R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107  
 R-HEMBA1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-UNIT VI REQUIRING PROTEIN [H.sapiens]/1.1e-72:350:99//Hs.116490:AA659584  
 35 R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939  
 R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997  
 R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353  
 R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193  
 R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540  
 40 R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239  
 R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521  
 R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692  
 R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915  
 45 R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951  
 R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223  
 R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558  
 R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965  
 R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353  
 50 R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364  
 R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019  
 R-HEMBA10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]/5.1e-73:449:89//Hs.16803:AA843214  
 55 R-HEMBA1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106  
 R-HEMBA1000244//Small inducible cytokine A5 (RANTES)/9.5e-42:323:83//Hs.155464:AF088219  
 R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783  
 R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

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R-HEM BB1000264  
R-HEM BB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]/2.7e-102:556:93//  
Hs.16079:AA083522  
R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385  
5 R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:  
AB011129  
R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458  
R-HEM BB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353  
R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601  
10 R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034  
R-HEM BB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219  
R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576  
R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480  
R-HEM BB-1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084  
15 R-HEM BB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219  
R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736  
R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651  
R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020  
R-HEM BB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008  
20 R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590  
R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.  
92381:AB007956  
R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969  
R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840  
25 R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642  
R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173  
R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026  
R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591  
R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087  
30 R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/0.30:214:63//  
Hs.142209:AA873303  
R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990  
R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221  
R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438  
35 R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396  
R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390  
R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506  
R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219  
R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080  
40 R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125  
R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703  
R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087  
R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080  
R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099  
45 R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662  
R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:  
AF052288  
R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986  
R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258  
50 R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709  
R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618  
R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247  
R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895  
R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704  
55 R-HEM BB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391  
R-HEM BB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199  
R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125  
R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

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R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152  
 R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531  
 R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522  
 R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582  
 5 R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963  
 R-HEM BB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100  
 R-HEM BB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939  
 R-HEM BB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988  
 R-HEM BB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705  
 10 R-HEM BB1000673//EST//0.58:46:82//Hs.142286:AA338293  
 R-HEM BB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454  
 R-HEM BB1000684//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723  
 R-HEM BB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219  
 R-HEM BB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412  
 15 R-HEM BB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403  
 R-HEM BB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306  
 R-HEM BB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881  
 R-HEM BB1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272  
 R-HEM BB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925  
 20 R-HEM BB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522  
 R-HEM BB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445  
 R-HEM BB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541  
 R-HEM BB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771  
 R-HEM BB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091  
 25 R-HEM BB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718  
 R-HEM BB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961  
 R-HEM BB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219  
 R-HEM BB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447  
 R-HEM BB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124  
 30 R-HEM BB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219  
 R-HEM BB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881  
 R-HEM BB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176  
 R-HEM BB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545  
 R-HEM BB1000840//ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876  
 35 R-HEM BB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137  
 R-HEM BB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599  
 R-HEM BB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942  
 R-HEM BB1000876//EST//0.0022:211:63//Hs.125552:AA884141  
 40 R-HEM BB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247  
 R-HEM BB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740  
 R-HEM BB1000888//EST//8.2e-07:196:64//Hs.118276:W15258  
 R-HEM BB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830  
 R-HEM BB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881  
 45 R-HEM BB1000908//EST//0.95:27:100//Hs.142568:AA285066  
 R-HEM BB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983  
 R-HEM BB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325  
 R-HEM BB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742  
 R-HEM BB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874  
 50 R-HEM BB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784  
 R-HEM BB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881  
 R-HEM BB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503  
 R-HEM BB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354  
 R-HEM BB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007  
 55 R-HEM BB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242  
 R-HEM BB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369  
 R-HEM BB1000991//EST//0.99:58:72//Hs.100246:T23625  
 R-HEM BB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

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R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112  
R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:  
H58762  
5 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214  
R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814  
R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080  
R-HEM BB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562  
R-HEM BB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385  
10 R-HEM BB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975  
R-HEM BB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107  
R-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:  
AB014518  
R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:  
AB007944  
15 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785  
R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381  
R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803  
R-HEM BB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:233:70//Hs.37181:D64108  
R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353  
20 R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080  
R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426  
R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092  
R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942  
R-HEM BB1001126  
25 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:  
285:73//Hs.554:M25077  
R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881  
R-HEM BB1001151  
30 R-HEM BB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-  
65:331:96//Hs.154179:AA579197  
R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878  
R-nnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162  
R-HEM BB1001177  
35 R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349  
R-HEM BB1001199  
R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183  
R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549  
R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573  
40 R-HEM BB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,  
antigen detected by monoclonal and antibody 1A4))//3.1e-44:298:87//Hs.103458:X53795  
R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817  
R-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//  
Hs.71873:AA148213  
45 R-HEM BB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560  
R-HEM BB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236  
R-HEM BB1001253//EST//0.0011:84:77//Hs.124579:AA853987  
R-HEM BB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268  
R-HEM BB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.  
50 159897:AB007970  
R-HEM BB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087  
R-HEM BB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412  
R-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III  
[Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021  
55 R-HEM BB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840  
R-HEM BB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112  
R-HEM BB1001302  
R-HEM BB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

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R-HEM BB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627  
R-HEM BB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627  
R-HEM BB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873  
5 R-HEM BB1001326//ESTs//0.85:174:62//Hs.133487:AI393754  
R-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222  
R-HEM BB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365  
R-HEM BB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639  
R-HEM BB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470  
10 R-HEM BB1001346  
R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354  
R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721  
R-HEM BB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055  
15 R-HEM BB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087  
R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617  
R-HEM BB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219  
R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205  
R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699  
20 R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970  
R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350  
R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342  
R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644  
R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651  
25 R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846  
R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317  
R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201  
R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236  
R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515  
30 R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293  
R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881  
R-HEM BB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468  
R-HEM BB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481  
R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515  
35 R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280  
R-HEM BB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915  
R-HEM BB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159  
40 R-HEM BB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459  
R-HEM BB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353  
R-HEM BB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869  
R-HEM BB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274  
R-HEM BB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962  
45 R-HEM BB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521  
R-HEM BB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329  
R-HEM BB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944  
R-HEM BB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219  
R-HEM BB1001588//EST//8.3e-27:363:69//Hs.141603:N66015  
50 R-HEM BB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184  
R-HEM BB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044  
R-HEM BB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888  
R-HEM BB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272  
R-HEM BB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082  
55 R-HEM BB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633  
R-HEM BB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813  
R-HEM BB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438  
R-HEM BB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

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R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572  
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546  
 R-HEMBB1001684//ESTs, Moderately similar to Tbcl [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534  
 5 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358  
 R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867  
 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038  
 R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080  
 10 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569  
 R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645  
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113  
 15 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403  
 R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488  
 R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287  
 R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059  
 R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211  
 20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352  
 R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369  
 R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406  
 R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253  
 25 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391  
 R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247  
 R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503  
 R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209  
 30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957  
 R-HEMBB1001839  
 R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125  
 R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539  
 35 R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106  
 R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397  
 R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434  
 R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980  
 R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572  
 40 R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240  
 R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081  
 R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310  
 R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191  
 R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725  
 45 R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915  
 R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216  
 R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750  
 R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897  
 R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390  
 50 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRp129//7.4e-38:531:70//Hs.153086:Y11251  
 R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325  
 R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875  
 R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366  
 55 R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875  
 R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589  
 R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998  
 R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

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R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522  
 R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881  
 R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972  
 R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:  
 5 AB011147  
 R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531  
 R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475  
 R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572  
 R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223  
 10 R-HEM BB1001996  
 R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798  
 R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:  
 K00627  
 R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334  
 15 R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896  
 R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052  
 R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900  
 R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426  
 R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638  
 20 R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080  
 R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638  
 R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840  
 R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671  
 R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.  
 25 129735:AF010144  
 R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193  
 R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881  
 R-HEM BB1002115  
 R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814  
 30 R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 1.4e-45:281:88//Hs.125231:AF068006  
 R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553  
 R-HEM BB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073  
 R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185  
 35 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934  
 R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881  
 R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841  
 R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584  
 R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631  
 40 R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807  
 R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503  
 R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363  
 R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112  
 R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223  
 45 R-HEM BB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892  
 R-HEM BB1002327//EST//0.042:249:61//Hs.121097:AA714637  
 R-HEM BB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEM BB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228  
 50 R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841  
 R-HEM BB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEM BB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613  
 R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522  
 R-HEM BB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085  
 55 R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467  
 R-HEM BB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055  
 R-HEM BB1002387  
 R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:



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168:77//Hs.133526:N21103  
R-HEM BB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280  
R-HEM BB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293  
5 R-HEM BB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353  
R-HEM BB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087  
R-HEM BB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089  
R-HEM BB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083  
R-HEM BB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176  
10 R-HEM BB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969  
R-HEM BB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017  
R-HEM BB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142  
R-HEM BB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615  
R-HEM BB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278  
15 R-HEM BB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538  
R-HEM BB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672  
R-HEM BB1002531//EST//0.024:147:61//Hs.148305:AA909605  
R-HEM BB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478  
20 R-HEM BB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259  
R-HEM BB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813  
R-HEM BB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830  
R-HEM BB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189  
25 R-HEM BB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045  
R-HEM BB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138  
R-HEM BB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087  
R-HEM BB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424  
R-HEM BB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923  
30 R-HEM BB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881  
R-HEM BB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896  
R-HEM BB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265  
R-HEM BB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977  
35 R-HEM BB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150  
R-HEM BB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917  
R-HEM BB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247  
40 R-HEM BB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219  
R-HEM BB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881  
R-HEM BB1002677//ESTs//0.65:159:62//Hs.163517:AI419775  
R-HEM BB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339  
45 R-HEM BB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646  
R-HEM BB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753  
R-HEM BB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099  
R-HEM BB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487  
R-HEM BB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398  
50 R-HEM BB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842  
R-HEM BB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547  
R-HEM BB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682  
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701  
R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219  
55 R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152  
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901  
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

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R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165  
 R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350  
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531  
 5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065  
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099  
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241  
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713  
 10 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352  
 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172  
 15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577  
 R-MAMMA1000133  
 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017  
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970  
 20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881  
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263  
 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787  
 R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162  
 25 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069  
 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611  
 R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054  
 30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881  
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103  
 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425  
 R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946  
 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315  
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090  
 R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041  
 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238  
 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814  
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977  
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369  
 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694  
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956  
 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000287  
 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892  
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067  
 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251  
 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434  
 R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491  
 55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998  
 R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881  
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

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R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159  
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912  
5 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087  
R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659  
R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523  
R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065  
R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132  
10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060  
R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973  
R-MAMMA1000410//Archair//1.8e-40:443:74//Hs.33642:X81198  
R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958  
15 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099  
R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171  
R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081  
20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067  
R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390  
R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452  
R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461  
25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171  
R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179  
R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447  
R-MAMMA1000458  
30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176  
R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361  
R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959  
R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886  
R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759  
35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219  
R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390  
R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390  
R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267  
R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236  
40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131  
R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561  
R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211  
R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872  
R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548  
45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219  
R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042  
R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267  
R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105  
50 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180  
R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361  
R-MAMMA1000623  
R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002  
55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203  
R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162  
R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

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R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/8.4e-98:464:98//Hs.31431:AI022065  
R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476  
R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212  
5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343  
R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644  
R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333  
R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/1.2e-29:158:79//Hs.142764:AA205569  
10 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515  
R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329  
R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942  
R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267  
15 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893  
R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]/1.2e-35:371:74//Hs.141429:AA631915  
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141  
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]/2.3e-116:557:98//Hs.71472:AA632288  
20 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205  
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503  
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627  
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131  
25 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256  
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353  
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204  
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439  
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150  
30 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163  
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)/1.5e-45:358:76//Hs.73919:X81637  
R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675  
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881  
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902  
35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/9.4e-44:363:79//Hs.96337:AA225358  
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097  
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955  
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251  
40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390  
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212  
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311  
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922  
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099  
45 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399  
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875  
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243  
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128  
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166  
50 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107  
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215  
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329  
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093  
55 R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634  
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989  
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

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R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335  
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727  
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281  
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428  
5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053  
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178  
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795  
10 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147  
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881  
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204  
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304  
15 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881  
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263  
R-MAMMA1001003//Sialoporphin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075  
20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313  
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333  
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814  
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536  
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461  
25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390  
R-nnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650  
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881  
R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487  
30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532  
R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748  
R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353  
R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944  
R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503  
35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222  
R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926  
R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587  
R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686  
40 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576  
R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267  
R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750  
45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029  
R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399  
R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179  
R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131  
R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750  
50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970  
R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251  
R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959  
R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519  
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202  
55 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348  
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637  
R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

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R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293  
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202  
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315  
 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701  
 5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619  
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307  
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569  
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149  
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561  
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001  
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643  
 15 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144  
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371  
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876  
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135  
 20 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426  
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984  
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709  
 25 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471  
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426  
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519  
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127  
 30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478  
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322  
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216  
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881  
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831  
 35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275  
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957  
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267  
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168  
 40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618  
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892  
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542  
 R-MAMMA1001465  
 45 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317  
 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394  
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065  
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522  
 R-MAMMA1001510  
 50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242  
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969  
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696  
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140  
 55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305  
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441  
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

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R-MAMMA1001604  
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616  
5 R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272  
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315  
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074  
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377  
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606  
10 R-MAMMA1001649  
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144  
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219  
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248  
15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550  
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081  
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957  
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884  
20 R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088  
R-MAMMA1001715//ESTs//1.2e-73:399:931//Hs.124620:AI082338  
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596  
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923:AI161158  
25 R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651  
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666  
R-MAMMA1001744  
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817  
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041  
30 R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413  
R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904  
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276  
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847  
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325  
35 R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825  
R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481246  
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460  
40 R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238  
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644  
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744  
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313  
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892  
45 R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659  
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979  
R-MAMMA1001818  
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881  
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519  
50 R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140  
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394  
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811  
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461  
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219  
55 R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840  
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944  
R-nnnnnnnnnnnn/Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

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AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

5 R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

10 R-nnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

15 R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

20 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

25 R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

30 R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:781//Hs.138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

35 R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

40 R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

45 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

50 R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

55 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540



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R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696  
R-MAMMA1002236  
R-MAMMA1002243  
5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080  
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript  
KIAA0487//1.6e-54:207:81//Hs.92381:AB007956  
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283  
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772  
10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141  
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751  
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982  
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881  
15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454  
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153  
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359  
R-MAMMA1002308  
20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452  
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503  
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094  
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280  
25 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183  
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084  
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658  
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317  
30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897  
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618  
R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439  
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127  
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228  
35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390  
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367  
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637  
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080  
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475  
40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587  
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236  
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542  
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219  
45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061  
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845  
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294  
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488  
50 R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588  
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477  
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475  
R-MAMMA1002434//ESTS, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348  
55 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996  
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

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89121:AB007954  
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076  
R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC  
REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106  
5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:  
263:79//Hs.38687:AA744496  
R-MAMMA10024807//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:  
159:79//Hs.133526:N21103  
10 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:  
AF055460  
R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293  
R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:  
U07664  
R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277  
15 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//  
3.9e-103:529:95//Hs.18858:AF065214  
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:  
AB011147  
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851  
20 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:  
280:65//Hs.12725:T65058  
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681  
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693  
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433  
25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371  
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258  
R-MAMMA1002597//Cytochrome P450, subfamily 1B (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//  
Hs.1360:M29874  
R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737  
30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369  
R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:  
75//Hs.1361:M55053  
R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389  
R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670  
35 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306  
R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081  
R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881  
R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.  
93332:AA811920  
40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.  
115325:D84488  
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390  
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421  
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915  
45 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776  
R-MAMMA1002655  
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886  
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087  
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:  
50 96//Hs.16464:W19606  
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213  
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:  
D86987  
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385  
55 R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675  
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510  
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:  
353:96//Hs.138404:R70986

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R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234  
 R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858  
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333  
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571  
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219  
 R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757  
 R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907  
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.  
 154069:U06452  
 10 R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:  
 369:77//Hs.105292:AA504776  
 R-MAMMA1002758  
 R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281  
 R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651  
 15 R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272  
 R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750  
 R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145  
 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812  
 R-MAMMA1002807//Archair//1.4e-39:315:80//Hs.33642:X81198  
 20 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260  
 R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319  
 R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881  
 R-MAMMA1002835  
 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723  
 25 R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395  
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238  
 R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081  
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067  
 R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941  
 30 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592  
 R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194  
 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871  
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219  
 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811  
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:  
 99//Hs.155871:AA533783  
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915  
 R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087  
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179  
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002  
 R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881  
 R-MAMMA1002938  
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503  
 R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243  
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353  
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081  
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630  
 R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835  
 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279  
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//  
 2.1e-41:402:67//Hs.133089:AF064019  
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179  
 R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857  
 R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617  
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.  
 92023:AI022248  
 R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189  
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

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R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315  
R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358  
5 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321  
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160  
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940  
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941  
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862  
10 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348  
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881  
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559  
R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911  
R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969  
15 R-MAMMA1003089//ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652  
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651  
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283  
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366  
20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788  
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125  
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537  
R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861  
25 R-nnnnnnnnnnnnn  
R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736  
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640  
R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312  
30 R-NT2RM4000027  
R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663  
R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169  
R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379  
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549:97//Hs.95665:AF070639  
35 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817  
R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708  
R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312  
R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:AI246301  
40 R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397  
R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962  
R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160  
R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113  
45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723  
R-NT2RM400019911ESTs//10.020:95:6511Hs.146203:AI254528  
R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876  
R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219  
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255  
50 R-NT2RM4000215  
R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760  
R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602  
55 R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031  
R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974  
R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

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R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891  
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520  
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:  
M21868  
5 R-NT2RM4000813  
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:  
AI219667  
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031  
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864  
10 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597  
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343  
R-nnnnnnnnnnn  
R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-  
96:450:99//Hs.142076:AA604514  
15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262  
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887  
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647  
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:  
AA650126  
20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:  
AB018272  
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:  
AB014539  
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352  
25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.  
32170:AB015132  
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300  
R-nnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798  
R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324  
30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962  
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276  
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311  
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848  
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085  
35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-  
43:273:91//Hs.109005:N31174  
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942  
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849  
R-NT2RM4001203  
40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307  
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410  
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677  
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184  
R-NT2RM4001309  
45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857  
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899  
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352  
R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.  
18442:AI129307  
50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339  
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476  
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211  
R-NT2RM4001382  
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507  
55 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790  
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:  
94//Hs.15744:AI055859  
R-NT2RM4001412

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R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895  
R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054  
R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]/7.4e-108:544:94//Hs.7558:AA526812  
5 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277  
R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739  
R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067  
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585  
10 R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664  
R-NT2RM40015227//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219  
R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]/6.1e-21:165:83//Hs.29134:H43072  
R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027  
15 R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046  
R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009  
R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946  
20 R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171  
R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871  
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334  
25 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079  
R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957  
R-NT2RM4001650  
R-NT2RM4001662  
R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938  
30 R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496  
R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440  
R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686  
R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]/3.1e-108:563:94//Hs.18510:AA522887  
35 R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]/0.083:124:68//Hs.120980:S83390  
R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200  
40 R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629  
R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740  
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270  
R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956  
R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567  
45 R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920  
R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839  
R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551  
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070  
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619  
50 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]/4.1e-10:274:62//Hs.161959:AA493652  
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]/3.0e-43:292:86//Hs.14202:N46000  
R-NT2RM40018657//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711  
55 R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252  
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149

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R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178  
R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438  
5 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143  
R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893  
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162  
R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268  
R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917  
10 R-NT2RM4001979//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097  
R-NT2RM4001984  
R-NT2RM4001987  
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528  
15 R-NT2RM4002018  
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087  
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435  
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226  
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887  
20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179  
R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629  
R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416  
25 R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655  
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528  
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620  
30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712  
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987  
R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090  
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535  
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258  
35 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400  
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343  
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678  
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079  
R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984  
40 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190  
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219  
R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864  
45 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263  
R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638  
R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461  
R-NT2RM4002294  
R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164  
50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498  
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198  
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549  
55 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594  
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884  
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328  
R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:



98//Hs.16464:W19606  
 R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677  
 R-NT2RM4002446  
 R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142  
 5 R-NT2RM4002457  
 R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890  
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.  
 8765:AF083255  
 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:  
 10 AB014591  
 R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884  
 R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029  
 R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//  
 15 Hs.31030:H50467  
 R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788  
 R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057  
 R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312  
 R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE [Bos  
 20 taurus]//2.3e-89:435:97//Hs.15830:AA165698  
 R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569  
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]  
 //9.6e-28:194:87//Hs.59346:AI126802  
 R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096  
 25 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081  
 R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115  
 R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713  
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 30 4.3e-64:309:98//Hs.6216:AF061749  
 R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798  
 R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910  
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:  
 AA775879  
 35 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881  
 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097  
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.  
 54877:AF050078  
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.  
 40 102576:AJ010230  
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338  
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064  
 R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757  
 R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827  
 45 R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419  
 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356  
 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 [C.elegans]//1.9e-19:153:86//Hs.5268:W22670  
 R-nnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099  
 50 R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513  
 R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-  
 89:457:95//Hs.3832:AI208601  
 R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548  
 R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820  
 55 R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190  
 R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741  
 R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373  
 R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

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R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897  
R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382  
R-NT2RP2000232  
5 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683  
R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379  
R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005  
R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840  
10 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649  
R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382  
R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635  
R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865  
15 R-NT2RP2000289  
R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249  
R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712  
R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381  
20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398  
25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441  
R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062  
R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981  
30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103  
R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010  
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324  
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265  
35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425  
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045  
R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013  
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078  
40 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215  
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896  
R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348  
R-NT2RP2000523  
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144  
45 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446  
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514  
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222  
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275  
R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396  
50 R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767  
R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347  
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368  
R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279  
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965  
55 R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642  
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419  
R-NT2RP2000809  
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

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R-nnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404  
 R-NT2RP2000816//ESTS//0.45:100:69//Hs.147529:AA458918  
 R-NT2RP2000819  
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511  
 5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6  
 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165  
 R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552  
 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345  
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:  
 10 AB018284  
 R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267  
 R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266  
 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III  
 [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477  
 15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:  
 AB018298  
 R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021  
 R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481  
 R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
 20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537  
 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521  
 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643  
 R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660  
 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108  
 25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665  
 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068  
 R-NT2RP2001119  
 R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348  
 R-NT2RP2001137  
 30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512  
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145  
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:  
 AB007949  
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287  
 35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510  
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402  
 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358  
 R-NT2RP2001233//TESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//  
 Hs.44014:AA632298  
 40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996  
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353  
 R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229  
 R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775  
 R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665  
 45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205  
 R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//  
 2.3e-43:238:93//Hs.106632:N25679  
 R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138  
 R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178  
 50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028  
 R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038  
 R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.  
 sapiens]//3.9e-74:411:93//Hs.47305:AA195153  
 R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875  
 55 R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:  
 469:97//Hs.20483:AA522505  
 R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030  
 R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

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R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728  
 R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:AI341556  
 R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394  
 R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453  
 5 R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765  
 R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539  
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219  
 R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513  
 R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146  
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:  
 Y14494  
 R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240  
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 1.9e-15:99:95//Hs.99742:AF035586  
 15 R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816  
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.  
 67619:AB007957  
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661  
 R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884  
 20 R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995  
 R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767  
 R-NT2RP2001613  
 R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294  
 R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090  
 25 R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845  
 R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336  
 R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323  
 R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579  
 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538  
 30 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100  
 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840  
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:  
 AF091754  
 R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037  
 35 R-NT2RP2001861  
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941  
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088  
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:  
 AA113849  
 40 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724  
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423  
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268  
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087  
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180  
 45 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594  
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588  
 R-NT2RP2001969  
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745  
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:  
 89//Hs.18760:AA166678  
 50 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233  
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332  
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627  
 R-NT2RP2002041  
 55 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938  
 R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895  
 R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068  
 R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091

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R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265  
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//Hs.11039:AF052183  
 R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524  
 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:89//Hs.155218:  
 5 AJ007509  
 R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000  
 R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134  
 R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527  
 R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268  
 10 R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495  
 R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859  
 R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-  
 15 15:245:71//Hs.87578:AI125363  
 R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:AI290672  
 R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946  
 R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499  
 R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341  
 R-nnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:  
 20 AA188168  
 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:  
 AF005418  
 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720  
 R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373  
 R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863  
 25 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//  
 Hs.24812:AF069532  
 R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015  
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:  
 30 95//Hs.31034:AB015594  
 R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372  
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:  
 89//Hs.109051:AF038958  
 R-NT2RP2002394//ESTS//0.11:158:65//Hs.28792:AI343467  
 R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815  
 35 R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:  
 AB011135  
 R-NT2RP2002439//ESTS//3.2e-12:134:76//Hs.32246:AA464020  
 R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521  
 R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230  
 40 R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233  
 R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.  
 125856:AB005289  
 R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180  
 R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838  
 45 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:  
 AB018334  
 R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305  
 R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090  
 R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:93//Hs.49476:AF009314  
 50 R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325  
 R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:  
 AA149547  
 R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783  
 R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170  
 55 R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220  
 R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615  
 R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881  
 R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

R-NT2RP2002672  
 R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572  
 R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223  
 R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210  
 5 R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626  
 R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300  
 R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108  
 R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352  
 R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131  
 10 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042  
 R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124  
 R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587  
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537  
 R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124  
 15 R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578  
 R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031  
 R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870  
 R-NT2RP2002880  
 20 R-NT2RP2002891  
 R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894  
 R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143  
 R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096  
 R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771  
 25 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480  
 R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060  
 R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213  
 R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291  
 30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329  
 R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311  
 R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642  
 R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594  
 35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082  
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081  
 R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512  
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345  
 R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355  
 40 R-NT2RP2003125  
 R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986  
 R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506  
 R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379  
 R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067  
 45 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952  
 R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156  
 R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816  
 R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074  
 R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253  
 50 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661  
 R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438  
 R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937  
 R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859  
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525  
 55 R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427  
 R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106  
 R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

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R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321  
R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874  
R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126  
5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948  
R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618  
R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825  
R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014  
R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476  
10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502  
R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249  
R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683  
R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073  
15 R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360  
R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903  
R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332  
R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121  
20 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777  
R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831  
R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733  
R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270  
25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783  
R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170  
R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101  
R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684  
30 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439  
R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696  
R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719  
R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463  
35 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067  
R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981  
R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188  
40 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951  
R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523  
R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:AI148540  
R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.93332:AA811920  
45 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246  
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097  
R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401  
R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003  
50 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003  
R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577  
R-NT2RP2003751  
R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808  
55 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709  
R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606  
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437

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R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811  
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838  
R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611  
10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.  
75875:U49278  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//  
Hs.35086:AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:  
15 AB007916  
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347  
R-NT2RP2003984  
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:  
20 AI149968  
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478  
R-NT2RP2004041  
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
R-nnnnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
25 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500  
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241  
30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:  
583:97//Hs.16520:AI224533  
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544  
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974  
R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
35 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
R-NT2RP2004196  
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:  
40 AA483305  
R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.  
54900:AF039687  
R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
45 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:  
50 AF000416  
R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
R-NT2RP2004347  
R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173  
R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310  
55 R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624  
R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192  
R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III  
[Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916



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R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646  
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473  
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900  
 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921  
 5 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121  
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124  
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695  
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PKD1) mRNA, complete cds//  
 8.6e-34:143:98//Hs.154729:AF017995  
 10 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700  
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320  
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081  
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347  
 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470  
 15 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661  
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126  
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666  
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862  
 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:  
 20 149:76//Hs.12845:N28835  
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:  
 AB007929  
 25 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930  
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:  
 AB014525  
 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793  
 30 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:  
 AB007947  
 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015  
 R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423  
 35 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774  
 R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 8.0e-116:564:96//Hs.40820:AF058953  
 R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579  
 40 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:  
 AF054179  
 R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906  
 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803  
 R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567  
 45 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529  
 R-NT2RP2004999//ESTs//0.059:137:64//Hs.144109:AI345543  
 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941  
 R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458  
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087  
 50 R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496  
 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910  
 R-NT2RP2004985  
 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902  
 R-NT2RP2005000  
 55 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:  
 AB014515  
 R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235  
 R-NT2RP2005003//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

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R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161  
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507  
 R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887  
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220  
 5 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757  
 R-NT2RP2005108  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564  
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743  
 10 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383  
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:AI341261  
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744  
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438  
 15 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582  
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648  
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509  
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166  
 20 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258  
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587  
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503  
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596  
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272  
 R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001  
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219  
 30 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590  
 R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261  
 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338  
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701  
 35 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699  
 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445  
 R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544  
 40 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247  
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304  
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697  
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631  
 45 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068  
 R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423  
 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096  
 R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307  
 50 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936  
 R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019  
 R-NT2RP2005476//ESTs//5.1 e-40:205:9811Hs.101577:AI168526  
 R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573  
 R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455  
 55 R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540  
 R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426  
 R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993

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R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755  
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME  
I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071  
5 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:  
570:9411Hs.119023:AF092563  
R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:  
433:95//Hs.36942:AA524535  
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856  
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:  
10 AJ012449  
R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:  
AB007963  
R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572  
R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567  
15 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169  
R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240  
R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733  
R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060  
R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788  
20 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229  
R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211  
R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740  
R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173  
R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:  
25 AA868470  
R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302  
R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987  
R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//  
Hs.25664:AF089814  
30 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229  
R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236  
R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643  
R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs.  
9095:AA532630  
35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:  
AB018342  
R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//  
Hs.14298:AI417523  
R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982  
40 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455  
R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153  
R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258  
R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064  
R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//  
45 Hs.159651:AF068868  
R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.  
26285:AF082516  
R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163  
R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463  
50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-  
112:559:96//Hs.14214:AI189379  
R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.  
22151:AI214321  
R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664  
55 R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724  
R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398  
R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746  
R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

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R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122  
 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403  
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062  
 R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462  
 5 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105  
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133  
 R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315  
 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268  
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:  
 10 94//Hs.16667:T92427  
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170  
 R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419  
 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988  
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080  
 15 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347  
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II  
 [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631  
 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492  
 R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714  
 20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093  
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918  
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//  
 Hs.46440:U21943  
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365  
 25 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522  
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258  
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435  
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:  
 AB014554  
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276  
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398  
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484  
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312  
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253  
 35 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928  
 R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999  
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262  
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015  
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:  
 40 N78664  
 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771  
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412  
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321  
 R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411  
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:  
 77//Hs.1361:M55053  
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.  
 115325:D84488  
 R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092  
 50 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146  
 R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595  
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266  
 R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478  
 R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679  
 55 R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947  
 R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474  
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886  
 R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

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R-nnnnnnnnnnn/ESTs//2.0e-112:533:98//Hs.18685:AI393829  
R-NT2RP2006598/ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112  
5 R-NT2RP3000002/ESTs//1.3e-08:399:59//Hs.126044:AI301598  
R-NT2RP3000031/Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972  
R-NT2RP3000046/Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219  
R-NT2RP3000047/EST//0.91:130:66//Hs.140208:AA702213  
10 R-NT2RP3000050/ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202  
R-NT2RP3000055/EST//2.4e-19:146:86//Hs.160497:AI255095  
R-NT2RP3000072/ESTs//2.2e-82:424:96//Hs.21542:N49574  
R-NT2RP3000080/ESTs//2.1e-29:186:89//Hs.153372:AA424029  
R-NT2RP3000085/ESTs//4.5e-101:482:98//Hs.47649:AA838715  
R-NT2RP3000109/ESTs//9.5e-97:455:99//Hs.17731:AI342241  
15 R-NT2RP3000134/EST//4.7e-106:497:99//Hs.125531:AA884000  
R-NT2RP3000142/Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164  
R-NT2RP3000149/ESTs//7.7e-62:361:90//Hs.6649:N93418  
R-NT2RP3000186  
20 R-NT2RP3000197/ESTs//1.5e-75:436:91//Hs.140931:R51882  
R-NT2RP3000207/ESTs//1.3e-98:468:98//Hs.126908:AA933091  
R-NT2RP3000220/ESTs//2.2e-27:144:99//Hs.106861:R61306  
R-NT2RP3000233/EST//7.8e-77:368:99//Hs.49075:N64817  
R-NT2RP3000235/ESTs//0.43:82:74//Hs.132828:AI032819  
25 R-NT2RP3000247/EST//2.2e-97:459:99//Hs.127928:AA969239  
R-NT2RP3000251  
R-NT2RP3000252/ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177  
R-NT2RP3000255/EST//0.67:93:67//Hs.120579:AA743073  
R-NT2RP3000267/ESTs//8.5e-108:542:95//Hs.24984:AA534446  
30 R-NT2RP3000299/ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323  
R-NT2RP3000312/ESTs//1.3e-100:493:97//Hs.29379:AI094117  
R-NT2RP3000320/ESTs//3.2e-95:538:91//Hs.118793:AA192438  
R-NT2RP3000324  
35 R-NT2RP3000333/ESTs//6.0e-39:194:100//Hs.119238:AA476267  
R-NT2RP3000341/ESTS//0.51:251:61//Hs.94090:AA777689  
R-NT2RP3000348/EST//1.8e-80:389:98//Hs.145944:AI276225  
R-NT2RP3000350/ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177  
R-NT2RP3000359/EST//4.9e-61:340:92//Hs.126495:AA913741  
40 R-NT2RP3000361/ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423  
R-NT2RP3000366/EST//0.20:392:57//Hs.149652:AI283303  
R-NT2RP3000397/EST//8.7e-26:150:94//Hs.124617:AA855106  
R-NT2RP3000403/Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185  
45 R-NT2RP3000418/EST//3.3e-09:202:67//Hs.117189:AA682947  
R-NT2RP3000433  
R-NT2RP3000439/ESTs//3.1e-79:426:92//Hs.26548:W26340  
R-NT2RP3000441/ESTs//6.3e-84:420:97//Hs.137482:AA421254  
50 R-NT2RP3000449/ESTs//4.9e-93:435:99//Hs.54617:AI379102  
R-NT2RP3000451/ESTs//2.3e-89:439:97//Hs.9196:AA748492  
R-NT2RP3000456/Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408  
R-NT2RP3000484/Heparin cofactor II//0.98:166:62//Hs.1478:M58600  
55 R-NT2RP3000487/ESTs//0.012:384:60//Hs.88684:AA885141  
R-NT2RP3000512/Homeo box B3//2.0e-69:377:93//Hs.49931:X16667  
R-NT2RP3000526/ESTS//1.6e-91:432:99//Hs.38042:AA187151  
R-NT2RP3000527/ESTs//1.2e-100:518:94//Hs.104557:AI078161

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R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]/0.95:85:71//Hs.5184:AA709151  
R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180  
R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036  
5 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071  
R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447  
R-NT2RP3000582//ESTS//2.1 e-25:131:80//Hs.152465:AA563785  
R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511  
R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817  
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916  
10 R-NNNNNNNNNNNN//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312  
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880  
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049  
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394  
R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]/5.4e-115:545:98//Hs.4857:AI090739  
15 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315  
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]/6.3e-92:434:99//Hs.152517:AA719022  
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084  
20 R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185  
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185  
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873  
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:AI085578  
R-NT2RP3000736  
25 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-ESTERASE DELTA 1 [Rattus norvegicus]/1.8e-07:114:75//Hs.136065:W21960  
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447  
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243  
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583  
30 R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810  
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582  
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081  
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082  
R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022  
35 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657  
R-NT2RP3000850  
R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272  
R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895  
R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741  
40 R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837  
R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673  
R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468  
R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217  
R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385  
45 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]/9.5e-113:566:96//Hs.5900:AA035728  
R-NT2RP3000919  
R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407  
R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178  
50 R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542  
R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405  
R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029  
R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044  
R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]/5.6e-102:486:99//Hs.145956:AA007349  
55 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)/0.0012:447:58//Hs.2133:U18991  
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874  
R-NT2RP3001096//ESTS//1.1e-110:540:96//Hs.42824:AA873182

R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832  
 R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325  
 R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:  
 C06063  
 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575  
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878  
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779  
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180  
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166  
 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188  
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761  
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305  
 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 //9.6e-113:552:97//Hs.23900:U82984  
 15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717  
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266  
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460  
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139  
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963  
 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196  
 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399  
 R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588  
 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:  
 AA524416  
 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631  
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997  
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135  
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857  
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965  
 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651  
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332  
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691  
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571  
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989  
 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:  
 U35234  
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:  
 AB007920  
 R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653  
 40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798  
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090  
 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778  
 R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//  
 Hs.96200:AA218942  
 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375  
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232  
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628  
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186  
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898  
 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817  
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158  
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692  
 R-nnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397  
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374  
 55 R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-  
 101:482:98//Hs.124135:AA910560  
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994  
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

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R-NT2RP3001457//ESTS//1.5e-52:256:99//Hs.117982:AA644658  
 R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280  
 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009  
 R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783  
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395  
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
 6.8e-112:549:9711Hs.28285:AF064801  
 R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047  
 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750  
 10 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463  
 R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:  
 AA524416  
 R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477  
 R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337  
 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194  
 R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328  
 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798  
 R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598  
 R-NT2RP3001629  
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149  
 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989  
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709  
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030  
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189  
 25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648  
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225  
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558  
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390  
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312  
 30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618  
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669  
 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
 //4.1e-80:444:91//Hs.6823:W18181  
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099  
 35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923  
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810  
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440  
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968  
 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:  
 40 N92517  
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725  
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:  
 AB007928  
 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900  
 45 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962  
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292  
 R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117  
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900  
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792  
 50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642  
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180  
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666  
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
 AI123300  
 55 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781  
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737  
 R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]  
 //1.3e-95:483:96//Hs.5771:W74591



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R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990  
R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325  
R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889  
R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:AI201540  
5 R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088  
R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779  
R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729  
R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219  
R-NT2RP3002033  
10 R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081  
R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426  
R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221  
R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486  
R-NT2RP3002062  
15 R-ntnnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657  
R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139  
R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148  
R-NT2RP3002102  
R-NT2RP3002108  
20 R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385  
R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703  
R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapi-  
ens]//6.2e-107:534:96//Hs.59523:AA602837  
R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293  
25 R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024  
R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713  
R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120  
R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598  
R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446  
30 R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588  
R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672  
R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743  
R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171  
R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898  
35 R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500  
R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]  
//1.8e-19:136:87//Hs.106928:AI041737  
R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667  
R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887  
40 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:  
Y16355  
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:  
AB014578  
R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486  
45 R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185  
R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III  
[C.elegans]//3.2e-90:526:90//Hs.8083:AA521436  
R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN  
C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246  
50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272  
R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673  
R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:  
184:63//Hs.89230:AF031815  
R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880  
55 R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850  
R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673  
R-NT2RP3002603  
R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

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R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365  
 R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573  
 R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172  
 5 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [*Drosophila melanogaster*]//5.9e-109:537:97//Hs.19348:AA151678  
 R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502  
 R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871  
 R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//5.0e-101:524:95//Hs.32580:AI123601  
 10 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169  
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945  
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159  
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973  
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958  
 15 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377  
 R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240  
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080  
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678  
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641  
 20 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262  
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314  
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286  
 25 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975  
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698  
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961  
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [*Saccharomyces cerevisiae*]112.0e-56:387:86//Hs.144597:W20143  
 30 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850  
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116  
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553  
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423  
 35 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [*Mus musculus*]//3.0e-100:528:94//Hs.90353:N98551  
 R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355  
 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912  
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [*C.elegans*]//5.9e-83:392:99//Hs.101364:AA534439  
 40 R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809  
 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466  
 R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441  
 R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520  
 R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982  
 45 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [*Mus musculus*]//3.3e-107:535:96//Hs.27437:AA004208  
 R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632  
 R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774  
 R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007  
 50 R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226  
 R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944  
 R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796  
 R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634  
 R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573  
 55 R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107  
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [*Dictyostelium discoideum*]//2.0e-40:229:93//Hs.17377:AI078151  
 R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

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R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628  
 R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960  
 R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061  
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983  
 5 R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035  
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055  
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818  
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261  
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931  
 10 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445  
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289  
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993  
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102  
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155  
 15 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567  
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272  
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721  
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095  
 20 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372  
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041  
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023  
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828  
 25 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268  
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:AI057529  
 30 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556  
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)<sub>n</sub>/(GTG)<sub>n</sub> repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952  
 R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430  
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681  
 35 R-NT2RP3003564  
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721  
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944  
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759  
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448  
 40 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957  
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310  
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714  
 R-NT2RP3003672  
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036  
 45 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768  
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923  
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 50 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913  
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446  
 55 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

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R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224  
R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:  
AF070611  
5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170  
R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
10 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221  
R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593  
R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
15 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
R-NT2RP3004041  
R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139  
R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537  
20 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-  
76:402:95//Hs.55847:W31092  
R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696  
25 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334  
R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093  
R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:  
200:100//Hs.26089:AA195126  
30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619  
R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE  
C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680  
R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794  
R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252  
35 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827  
R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628  
R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:  
468:95//Hs.5117:AA831530  
R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623  
40 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630  
R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264  
R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258  
R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223  
R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044  
45 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224  
R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934  
R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985  
R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621  
R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:  
50 AB007917  
R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616  
R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332  
R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406  
R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925  
55 R-NT2RP3004480  
R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504  
R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.  
47393:AA218858

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R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//  
1.8e-83:465:92//Hs.137064:AA318257  
R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
5 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
R-nnnnnnnnnnnnn  
R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
10 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
15 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase  
(GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680  
R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
20 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266  
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945  
R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
25 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:  
AB007952  
R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III  
30 [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569  
R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:  
35 AB014600  
R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390  
R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:  
40 AJ006470  
R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:  
AF091092  
R-NT2RP4000263  
45 R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]  
//4.7e-104:525:96//Hs.152069:AA548972  
R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631  
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524  
R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760  
50 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390  
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:  
AB018281  
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-  
110:527:98//Hs.31323:AF044195  
55 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130  
R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498  
R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376  
R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

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91//Hs.26156:AA630975  
R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTER-  
GENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:AI191318  
5 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011  
R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955  
R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953  
R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-  
plete cds//0.35:153:63//Hs.113286:U77783  
10 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167  
R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III  
[C.elegans]//1.2e-40:125:97//Hs.56124:AI424792  
R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713  
15 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868  
R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874  
R-NT2RP4000519  
R-NT2RP4000524//ESTS, Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:H07126  
R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213  
20 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328  
R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//Hs.  
25597:H93026  
R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840  
R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263  
25 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531  
R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393  
R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704  
R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651  
R-NT2RP4000724//ESTS//1.5e-83:442:94//Hs.142114:AA205615  
30 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399  
R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211  
R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312  
R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:  
AB007939  
35 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834  
R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028  
R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104  
R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356  
R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185  
40 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617  
R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:85//Hs.14146:W92235  
R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//  
45 Hs.24812:AF069532  
R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905  
R-NT2RP4000955//ESTs//3.5e-10:19:78//Hs.42946:N21111  
R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986  
50 R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179  
R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017  
R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123  
R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018  
R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620  
55 R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-28:439:68//Hs.  
129735:AF010144  
R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769  
R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-124:574:99//Hs.

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R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511  
 R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385  
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863  
 R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292  
 5 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium  
 tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928  
 R-ntnnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:  
 88//Hs.136189:AA133224  
 R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552  
 10 R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285  
 R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437  
 R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251  
 R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906  
 R-NT2RP4001575  
 15 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]  
 //8.7e-112:557:97//Hs.7558:AA526812  
 R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776  
 R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657  
 R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737  
 20 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:  
 AF007151  
 R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361  
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II  
 [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734  
 25 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805  
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.  
 15562:U96629  
 R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941  
 R-ntnnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-  
 30 CURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922  
 R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692  
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926  
 R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315  
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:  
 35 W28098  
 R-NT2RP4001803  
 R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133  
 R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434  
 R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826  
 40 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087  
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528  
 45 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606  
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099  
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
 R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793  
 50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637  
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:  
 AA775879  
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
 R-NT2RP4002018  
 55 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:  
 90:86//Hs.41127:AA555184  
 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106



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R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679  
R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198  
R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507  
5 R-nnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565  
R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407  
R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592  
R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555  
10 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272  
R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090  
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934  
15 R-OVARC1000004  
R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929  
R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635  
R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273  
R-OVARC1000017  
20 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286  
R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073  
R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041  
R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367  
R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787  
25 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259  
R-nnnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703  
R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370  
R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942  
30 R-OVARC1000106  
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250  
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312  
R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482  
35 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214  
R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090  
R-OVARC1000151  
R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023  
R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629  
40 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258  
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864  
R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874  
R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958  
45 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130  
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079  
R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476  
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777  
50 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449  
R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743  
R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682  
55 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863  
R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672  
R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423  
R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

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R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 5 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//  
 Hs.73614:U83460  
 10 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:  
 AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576  
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211  
 15 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 20 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219  
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248  
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021  
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106  
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285  
 25 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587  
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627  
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219  
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053  
 R-OVARC1000605  
 30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.  
 159897:AB007970  
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073  
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:  
 AB011162  
 35 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480  
 R-nnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522  
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875  
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517  
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901  
 40 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461  
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-  
 45 28:430:69//Hs.42457:AA523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066  
 50 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:  
 Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637  
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584  
 55 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096  
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292  
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

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REGION [Bacillus subtilis]/7.9e-98:525:93//Hs.10366:W21953  
 R-OVARC1000886//ESTs/8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs/6.8e-75:401:94//Hs.5833:H15401  
 R-OVARC1000897//ESTs/3.5e-91:440:98//Hs.125264:AA873350  
 5 R-OVARC1000912  
 R-OVARC1000915//ESTs/1.0e-45:328:82//Hs.163980:AA715814  
 R-OVARC1000924//ESTs/1.0e-100:501:96//Hs.30204:AA497127  
 R-OVARC1000936//EST/3.0e-74:367:98//Hs.145098:AA421696  
 R-OVARC1000937//EST/1.1e-53:290:95//Hs.162846:AA631215  
 10 R-OVARC1000945//ESTs/4.9e-51:301:89//Hs.20100:W25794  
 R-OVARC1000948//ESTs/3.7e-67:332:98//Hs.112570:AA621971  
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)/7.2e-44:283:86//Hs.155464:AF088219  
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds/1.1e-41:348:80//Hs.43681:AL022394  
 R-OVARC1000971//EST/6.2e-05:126:70//Hs.160491:AI254909  
 15 R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]/3.5e-68:346:96//Hs.25544:AA532784  
 R-OVARC1000996//EST/0.12:92:71//Hs.117141:AA678811  
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds/1.5e-44:513:73//Hs.127649:AB007874  
 R-OVARC1001000//ESTs/1.8e-22:198:80//Hs.140608:N53448  
 20 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end/1.7e-28:181:77//Hs.139107:K00629  
 R-OVARC1001010//EST/2.1e-09:92:85//Hs.147893:AI223270  
 R-OVARC1001011//EST/2.4e-14:200:75//Hs.149290:AI248117  
 R-OVARC1001032//EST/2.7e-29:304:73//Hs.141733:W80630  
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds/2.1e-09:  
 25 137:74//Hs.77579:AF013263  
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds/4.1e-101:501:96//Hs.9899:AF099149  
 R-OVARC1001040//ESTs/2.9e-87:415:99//Hs.132812:AI032046  
 R-OVARC1001044//ESTs/1.1e-83:432:96//Hs.55043:N94384  
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41/1.2e-16:124:88//Hs.108124:Z12962  
 30 R-OVARC1001055//ESTs/2.4e-23:238:76//Hs.141421:H99231  
 R-OVARC1001062//ESTs/3.4e-92:469:96//Hs.34658:N98652  
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds/7.3e-97:463:98//Hs.3426:AF082657  
 R-OVARC1001072//ESTs/1.3e-34:227:89//Hs.126704:W95844  
 35 R-OVARC1001074  
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor/1.0:94:69//Hs.103126:U57029  
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))/1.4e-96:325:98//Hs.21753:AJ005897  
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds/3.3e-75:386:95//Hs.26584:AF051782  
 40 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds/3.9e-37:283:84//Hs.46468:U45984  
 R-OVARC1001118//ESTs/5.3e-99:485:97//Hs.130815:AA936548  
 R-OVARC1001129//ESTs/9.8e-66:351:95//Hs.18616:T99312  
 45 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]/2.2e-66:346:95//Hs.53263:AA173226  
 R-OVARC1001162//EST/1.5e-44:376:80//Hs.161917:AA483223  
 R-OVARC1001167//ESTs/4.7e-110:548:96//Hs.35254:AI133727  
 R-OVARC1001169//ESTs/0.22:152:68//Hs.149424:AI274200  
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)/1.8e-42:305:84//Hs.155464:AF088219  
 R-OVARC1001173//EST/2.5e-35:182:84//Hs.161917:AA483223  
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds/6.6e-64:247:80//Hs.97203:U83171  
 R-OVARC1001188//ESTs/4.1e-18:296:69//Hs.139197:AA228343  
 55 R-OVARC1001200//ESTs/2.0e-28:207:85//Hs.35121:AA877826  
 R-OVARC1001232//ESTs/3.2e-61:358:91//Hs.6449:W95025  
 R-OVARC1001240//ESTs/6.7e-45:316:85//Hs.121675:AA629668  
 R-OVARC1001243//ESTs/2.3e-86:409:99//Hs.163091:AA742361

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R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166  
 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929  
 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708  
 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532  
 5 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113  
 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:  
 AB011090  
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637  
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344  
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219  
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-  
 85:464:93//Hs.23651:AA650356  
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247  
 15 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216  
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657  
 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844  
 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777  
 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415  
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:  
 AB011147  
 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958  
 R-OVARC1001391  
 R-nnnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913  
 25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651  
 R-OVARC1001419  
 R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136  
 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427  
 R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345  
 30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592  
 R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700  
 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694  
 R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089  
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:  
 35 AF016507  
 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219  
 R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539  
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492  
 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388  
 40 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7/4.4e-20:150:89//Hs.155160:  
 AF031166  
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087  
 R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019  
 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965  
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869  
 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659  
 R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854  
 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080  
 R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784  
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:  
 AA046954  
 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276  
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:  
 AF057280  
 55 R-nnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:  
 540:92//Hs.117741:AA903456  
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 1.1e-109:567:94//Hs.155377:U97670

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R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575

R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127

R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604

5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978

R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333

R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688

R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831

R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110

10 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621

R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160

R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:AF070611

15 R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476

R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147

R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

25 R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892

30 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531

35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934

R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315

40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860

R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691

R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825

45 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923

R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631

R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160

R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478

R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337

50 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557

R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223

R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870

55 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440

R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503

R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

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R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-61:331:94//Hs.30026:AI356771  
R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659  
R-PLACE1000081  
5 R-PLACE1000094  
R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505  
R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:AA632135  
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291  
10 R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:W22072  
R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946  
R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916  
15 R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077  
R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545  
R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912  
R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940  
R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424  
20 R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126  
R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994  
R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708  
R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959  
R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089  
25 R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799  
R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125  
R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131  
R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456  
30 R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118  
R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793  
R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [H.sapiens]//3.2e-109:549:95//Hs.19074:U69566  
R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425  
35 R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729  
R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:AB014540  
R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//Hs.163791:W25348  
40 R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485  
R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353  
R-nnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542  
R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030  
45 R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087  
R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301  
R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308  
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265  
50 R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896  
R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353  
R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485  
55 R-PLACE1000716  
R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701  
R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396  
R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.el-

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egans//3.9e-40:224:94//Hs.87889:AA262008  
R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536  
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548  
5 R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482  
R-nnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219  
R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189  
R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135  
10 R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588  
R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039  
R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118:-AI141558  
R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846  
15 R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091  
R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697  
R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941  
R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689  
R-PLACE1000979  
20 R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725  
R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361  
R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146  
R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878  
R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736  
25 R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762  
R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120  
R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124  
R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580  
R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141  
30 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268  
R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610  
R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594  
R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834  
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527  
35 R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297  
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812  
R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464  
40 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131  
R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371  
R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780  
R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460  
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548  
45 R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601  
R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056  
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160  
50 R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077  
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219  
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615  
55 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030  
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419  
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

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R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087  
 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
 R-PLACE1001440  
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.  
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547  
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625  
 10 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617  
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
 R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969  
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153  
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265  
 15 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601  
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
 20 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174  
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095  
 25 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526  
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
 R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804  
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250  
 30 R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124  
 R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903  
 R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667  
 R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993  
 35 R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171  
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113  
 R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266  
 R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479  
 R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937  
 40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243  
 R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662  
 R-PLACE1001761  
 R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980  
 45 R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236  
 R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463:95//Hs.40820:AF058953  
 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219  
 50 R-PLACE1001845  
 R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868  
 R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009  
 R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098  
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936  
 55 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:AB014523  
 R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313



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R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941  
 R-PLACE1002046  
 R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595  
 R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094  
 5 R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619  
 R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552  
 R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632  
 R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311  
 R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293  
 10 R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937  
 R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614  
 R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189  
 R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965  
 15 R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745  
 R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793  
 R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788  
 R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892  
 R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257  
 20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503  
 R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308  
 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271  
 R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291  
 R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381  
 25 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
 R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
 R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804  
 R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
 R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320  
 30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263  
 R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
 R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
 35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869  
 R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256  
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774  
 40 R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
 R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437  
 R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
 R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738  
 45 R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
 R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208  
 R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147  
 R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
 50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180  
 R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
 R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586  
 55 R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865  
 R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099  
 R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

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R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955  
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392  
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.  
 61518:AA167094  
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756  
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762  
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332  
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
 R-PLACE1002962  
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
 R-PLACE10029937//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:  
 502:89//Hs.32232:AA604268  
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268  
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499  
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075  
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:  
 U04840  
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777  
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.  
 25 6318:AI131178  
 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359  
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920  
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757  
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467  
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924  
 R-PLACE1003176  
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453  
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017  
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802  
 35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123  
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//  
 Hs.73614:U83460  
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131  
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:  
 40 551:92//Hs.52431:AA625326  
 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986  
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.  
 29147:AA883993  
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:  
 45 97//Hs.155050:AA908765  
 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438  
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701  
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 cds//1.1e-99:469:98//Hs.6564:U92715  
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636  
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234  
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591  
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941  
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909  
 55 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755  
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020  
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840  
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

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R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671  
 R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270  
 R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952  
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505  
 5 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980  
 R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461  
 R-PLACE1003537//ESTs, Weakly similar to multispinning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209  
 R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321  
 10 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591  
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956  
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178  
 15 R-PLACE1003584  
 R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542  
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106  
 R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875  
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200  
 20 R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299  
 R-PLACE1003618//ESTs//1.0:78:71//Hs.101248:T26446  
 R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943  
 R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285  
 R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247  
 25 R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607  
 R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521  
 R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866  
 R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639  
 R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987  
 30 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087  
 R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023  
 R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512  
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965  
 R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798  
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757  
 R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909  
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147  
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092  
 40 R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059  
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058  
 R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871  
 45 R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595  
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915  
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259  
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804  
 50 R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760  
 R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236  
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110  
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567  
 55 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330  
 R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231  
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052  
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

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R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244  
 R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714  
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080  
 R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601  
 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//  
 4.7e-78:434:91//Hs.153504:AF044321  
 R-PLACE1004197  
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//  
 1.5e-105:501:98//Hs.24640:AF069493  
 10 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952  
 R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630  
 R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209  
 R-PLACE1004258//KERATIN. TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124  
 R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800  
 15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:  
 121:66//Hs.1938:S82362  
 R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//1.4e-107:581:  
 91//Hs.127007:AF084830  
 R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114  
 20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:  
 279:77//Hs.38687:AA744496  
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.  
 71435:AI253099  
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588  
 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:  
 77//Hs.1361:M55053  
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:  
 379:93//Hs.16232:AF100153  
 R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309  
 30 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556  
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-  
 98:572:90//Hs.14202:N46000  
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467  
 R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665  
 35 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
 R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283  
 R-PLACE1004451  
 R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980  
 40 R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721  
 R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578  
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194  
 R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:  
 278:61//Hs.89663:L13286  
 45 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117  
 R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493  
 R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164  
 R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553  
 R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.  
 50 115325:084488  
 R-PLACE1004550  
 R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742  
 R-PLACE1004629//ESTs, Weakly similar to OS-9 precurosor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181  
 R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903  
 55 R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734  
 R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113  
 R-nnnnnnnnnnnn/Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257  
 R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

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R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs.80019:AF035606  
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482  
R-PLACE1004686  
5 R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552  
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374  
R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:AI279571  
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997  
10 R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391  
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619  
R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195  
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374  
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367  
15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548  
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178  
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856  
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250  
20 R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356  
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663  
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185  
25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299  
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901  
R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381:93//Hs.8383:AA013272  
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308  
30 R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456  
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881  
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597  
R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563  
35 R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948  
R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936  
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980  
R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166  
40 R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013  
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106  
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789  
R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776  
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335  
45 R-PLACE1005026  
R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719  
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147  
50 R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605  
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103  
R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985  
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080  
55 R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364  
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531:92//Hs.75437:L40401  
R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336  
R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

U91985

- R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225  
 R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423  
 R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349  
 5 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013  
 R-nnnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227  
 R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589  
 R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830  
 R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211  
 10 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532  
 R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767  
 R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524  
 R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633  
 R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516  
 15 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322  
 R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937  
 R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797  
 R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614  
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960  
 20 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343  
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975  
 R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901  
 R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394  
 R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978  
 25 R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304  
 R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423  
 R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503  
 R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607  
 R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046  
 30 R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875  
 R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220  
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185  
 R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325  
 35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470  
 R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325  
 R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927  
 40 R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555  
 R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261  
 R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835  
 R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612  
 45 R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023  
 R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927  
 R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857  
 R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964  
 R-PLACE1005630  
 50 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452  
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255  
 R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169  
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587  
 55 R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355  
 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332  
 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

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R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137  
R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070  
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087  
5 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.109857:AA088385  
R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941  
R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327  
R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693  
10 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058  
R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870  
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965  
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471  
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305  
15 R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842  
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558  
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981  
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501  
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793  
20 R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503  
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361  
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142  
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913  
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729  
25 R-PLACE1005953  
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:AI097079  
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239  
R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897  
30 R-PLACE1005990  
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353  
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:AI192946  
R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-100:596:88//Hs.24284:AA595596  
35 R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276  
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164:AI096332  
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765  
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314  
40 R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904  
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002  
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977  
45 R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:59//Hs.904:U84010  
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886  
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925  
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128  
50 R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239  
R-nnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:AI125280  
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433  
R-PLACE1006195//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:AI361807  
55 R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507  
R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114  
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664

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R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555  
 R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472  
 R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142  
 5 R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532:95//Hs.41151:AI301961  
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548  
 R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839  
 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132  
 10 R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265  
 R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503  
 R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900  
 R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168  
 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044  
 15 R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284  
 R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053  
 R-PLACE1006382  
 R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748  
 R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881  
 20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258  
 R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629  
 R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139  
 R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961  
 R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297  
 25 R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418  
 R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722  
 R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374  
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717  
 R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723  
 30 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368  
 R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532  
 R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214  
 R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 35 9.3e-118:590:95//Hs.155377:U97670  
 R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322  
 R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615  
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384  
 R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522  
 40 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627  
 R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736  
 R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214  
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172  
 R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861  
 45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622  
 R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658  
 R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234  
 R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515  
 R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335  
 50 R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989  
 R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847  
 R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159  
 R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
 1.0e-87:481:92//Hs.141263:H64113  
 55 R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933  
 R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA-828359  
 R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008  
 R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536



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R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131  
 R-nnnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348  
 R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089  
 R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168  
 5 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514  
 R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078  
 R-nnnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956  
 R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520  
 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982  
 10 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636  
 R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257  
 R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366  
 R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971  
 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503  
 15 R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575  
 R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027  
 R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202  
 R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646  
 R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417  
 20 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948  
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794  
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765  
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998  
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619  
 25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495  
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450  
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499  
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909  
 30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071  
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087  
 R-PLACE1007301  
 35 R-PLACE1007317  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594  
 40 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945  
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877  
 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771  
 45 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857  
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171  
 50 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514  
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230  
 R-PLACE1007478  
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975  
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533  
 55 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072  
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657

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R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377  
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087  
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612  
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404  
 5 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840  
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179  
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176  
 10 R-PLACE1007632  
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106  
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946  
 R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//  
 9.0e-37:190:97//Hs.23437:AA707331  
 15 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944  
 R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]  
 //3.4e-61:384:89//Hs.92918:AA133274  
 R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.  
 91251:U66685  
 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:  
 AF061243  
 R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:  
 AA476815  
 25 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:  
 AB014585  
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322  
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778  
 30 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903  
 R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
 8.6e-27:143:98//Hs.144194:AA706337  
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503  
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044  
 35 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050  
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839  
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503  
 R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:  
 40 AB018309  
 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178  
 R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832  
 R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060  
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.  
 45 92381:AB007956  
 R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510  
 R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966  
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.  
 5671:AF084530  
 50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:  
 465:93//Hs.78106:AF079529  
 R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900  
 R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]  
 //3.8e-97:493:95//Hs.6141:U69564  
 55 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835  
 R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612  
 R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]  
 //2.0e-115:575:95//Hs.92395:AA779854

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R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935  
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269  
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469  
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334  
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617  
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266  
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
 R-aaaaaaaaaaaaa/Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102  
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701  
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
 R-aaaaaaaaaaaaa  
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705  
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276  
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//  
 Hs.146477:AI128445  
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579  
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052  
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-  
 41:448:72//Hs.139007:H74314  
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242  
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:  
 30 536:87//Hs.7570:W31010  
 R-aaaaaaaaaaaaa/Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326  
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778  
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387  
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636  
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816  
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
 R-PLACE1008532  
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223  
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064  
 R-PLACE1008621//ESTS, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:  
 AA778649  
 R-aaaaaaaaaaaaa  
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
 R-PLACE1008627//ESTS//1.6e-90:475:93//Hs.102401:AI004972  
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512  
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612  
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353  
 55 R-PLACE10086507/Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.  
 147967:AF044333  
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830  
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

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76//Hs.1361:M55053  
R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600  
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303  
5 R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408  
R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313  
R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930  
R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217  
R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905  
10 R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810  
R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428  
R-nnnnnnnnnnnnn  
15 R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502  
R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878  
R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893  
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308  
R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018  
20 R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653  
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680  
R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573  
R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419  
25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112  
R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520  
R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195  
R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139  
R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008  
30 R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142  
R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448  
R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546  
R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136  
35 R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549  
R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983  
R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945  
R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747  
40 R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920  
R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005  
R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322  
R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948  
45 R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707  
R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717  
R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396  
R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701  
50 R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248  
R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680  
R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018  
R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423  
R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279  
55 R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503  
R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397  
R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782  
R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

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R-PLACE1009375//ESTs//8.9e-313:76//Hs.24608:AA161260  
R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883  
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186  
R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798  
5 R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255  
R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632  
R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269  
R-PLACE1099444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872  
R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427  
10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:  
AC004531  
R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925  
R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596  
R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698  
15 R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131  
R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:  
289:63//Hs.77579:AF013263  
R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326  
R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.  
20 sapiens]//0.0012:56:91//Hs.12151:AA001818  
R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:  
AB014535  
R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735  
R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482  
25 R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680  
R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338  
R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858  
R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701  
R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213  
30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:  
AB011159  
R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:  
AA778649  
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534  
35 R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:N48582  
R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210  
R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.  
26194:AA033989  
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024  
40 R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989  
R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene  
Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-  
45 113:549:97//Hs.16411:AL030996  
R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868  
R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748  
R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328  
R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031  
50 R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:  
AI219740  
R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563  
R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276  
R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317  
55 R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543  
R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074  
R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540  
R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

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R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347  
R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219  
R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]/1.7e-17:137:86//Hs.7049:  
AI141736  
5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204  
R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]/  
7.6e-104:546:94//Hs.8215:AA521150  
R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905  
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.  
10 11183AF065482  
R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375  
R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424  
R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615  
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]/2.8e-104:565:92//Hs.11469:  
15 U69567  
R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015  
R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103  
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]/1.6e-107:575:93//Hs.48301:AA122270  
R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130  
20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359  
R-PLACE1010152//ESTS//1.9e-40:240:90//Hs.17054:AI139897  
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313  
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466  
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037  
25 R-PLACE1010231  
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478  
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545  
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535  
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788  
30 R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081  
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568  
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219  
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]/9.9e-  
32:190:77//Hs.152369:AA504818  
35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327  
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594  
R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:  
AJ224162  
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152  
40 R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816  
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:  
AF039081  
R-PLACE1010492  
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031  
45 R-nnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455  
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306  
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033  
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116  
R-PLACE1010599  
50 R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418  
R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895  
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475  
R-PLACE1010628//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/6.4e-74:  
391:95//Hs.163495:W57637  
55 R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805  
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719  
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102  
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]/4.8e-83:467:

91//Hs.22383:R51067  
 R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]/8.3e-103:538:94//Hs.105794:AA701659  
 R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973  
 5 R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//  
 Hs.46440:U21943  
 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:  
 95//Hs.50758:AF092564  
 R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189  
 10 R-PLACE1010743  
 R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-  
 94:442:96//Hs.3688:AF069250  
 R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024  
 R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]/7.6e-111:575:  
 15 94//Hs.10260:AI126627  
 R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558  
 R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:AI091203  
 R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896  
 R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472  
 20 R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048  
 R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]/1.4e-71:326:92//Hs.3385:N25917  
 R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090  
 R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:  
 AB011182  
 25 R-PLACE1010891  
 R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983  
 R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023  
 R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630  
 R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093  
 30 R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479  
 R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126  
 R-nnnnnnnnnnnn/Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:  
 AF064244  
 R-PLACE1010944  
 35 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519  
 R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219  
 R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]/1.0e-103:565:  
 92//Hs.23259:AA532437  
 R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580  
 40 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846  
 R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867  
 R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249  
 R-nnnnnnnnnnnn/Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153  
 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135  
 45 R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219  
 R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537  
 R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.6e-54:  
 398:84//Hs.108740:W20094  
 R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478  
 50 R-PLACE101111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587  
 R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]/3.0e-105:552:93//Hs.31257:  
 AA875998  
 R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795  
 R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333  
 55 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673  
 R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]/3.4e-85:442:  
 95//Hs.136910:AA810782  
 R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

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R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.14834:AI138671  
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299  
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693  
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602  
5 R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772  
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913  
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849  
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807  
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291  
10 R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578  
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337  
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376  
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194  
15 R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102  
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607  
20 R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887  
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255  
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278  
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294  
25 R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576  
R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421  
R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985  
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672  
R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548  
30 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067  
R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965  
R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900  
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535  
R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036  
35 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838  
R-PLACE1011675  
R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025  
R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503  
40 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392  
R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426  
R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:Z48051  
R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627  
45 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179  
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067  
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
50 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497  
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617  
55 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969  
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285  
R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890



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R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256  
R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
5 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080  
R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504  
10 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868  
R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452  
R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073  
15 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622  
R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652  
R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147  
20 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390  
R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219  
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179  
R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236  
25 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941  
R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789  
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662  
R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988  
30 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558  
R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134  
R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357  
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219  
35 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778  
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292  
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067  
R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378  
R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191  
40 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717  
R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600  
R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363  
R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:AI004779  
45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664  
R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055  
R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380  
R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058  
50 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789  
R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618  
R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848  
R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081  
55 R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731  
R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277  
R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781  
R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

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R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189  
R-PLACE2000399  
R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424  
5 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941  
R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739  
R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333  
R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002  
10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523  
R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986  
R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887  
R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390  
R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714  
15 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638  
R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228  
R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642  
R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838  
R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:  
20 AB011147  
R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763  
R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979  
R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830  
R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727  
25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739  
R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792  
R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369  
R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142  
R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815  
30 R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223  
R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//  
Hs.31532:H18272  
R-PLACE3000157  
R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219  
35 R-PLACE3000160  
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
R-PLACE3000194  
R-PLACE3000197//ESTs//1.4e-3 8:197:98//Hs.146341:AI269930  
R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.  
40 131370:AA927516  
R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084  
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964  
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014  
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878  
R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811  
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-  
110:549:95//Hs.13692:AA632002  
50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307  
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:  
82//Hs.97203:U83171  
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-  
55 plete cds//4.0e-59:456:80//Hs.108966:U48696  
R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830  
R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627  
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

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114531:N74103  
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:  
AB018315  
R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837  
5 R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688  
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377  
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380  
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683  
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888  
10 R-PLACE3000363  
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881  
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430  
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-  
35:427:73//Hs.138795:R98534  
15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570  
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528  
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230  
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160  
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108  
20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//  
Hs.73614:U83460  
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077  
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219  
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519  
25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461  
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.  
153487:U43899  
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980  
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227  
30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:  
AB018352  
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240  
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031  
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292  
35 R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444  
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547  
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739  
R-PLACE4000100  
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:  
40 AB007931  
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-  
11:184:71//Hs.154278:N45985  
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.  
118164:AB007969  
45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582  
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:  
AB011147  
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:  
232:82//Hs.16493:T92186  
50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734  
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949  
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080  
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219  
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216  
55 R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442  
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586  
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:  
352:77//Hs.77579:AF013263

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R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782  
 R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131  
 R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454  
 R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460  
 5 R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414  
 R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478  
 R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656  
 R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425  
 R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-  
 10 44:379:78//Hs.152369:AA504818  
 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:  
 AA778649  
 R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502  
 R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780  
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:  
 AA643063  
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:  
 72//Hs.1361:M55053  
 R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932  
 20 R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210  
 R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290  
 R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527  
 R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//  
 Hs.23590:U59185  
 25 R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532  
 R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524  
 R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249  
 R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889  
 R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651  
 30 R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438  
 R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435  
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353  
 R-THYRO1000107//Interleukin 10//2.8e-43:292:84//Hs.2180:M57627  
 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
 35 1.0e-52:413:80//Hs.140385:AA773359  
 R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108  
 R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764  
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:  
 AF087142  
 40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-  
 49:486:77//Hs.24164:N95217  
 R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426  
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258  
 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-  
 45 111:554:96//Hs.18894:AA910946  
 R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189  
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219  
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219  
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:  
 50 AJ005698  
 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:  
 AB014552  
 R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063  
 R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING  
 55 ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349  
 R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:  
 AB014588  
 R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075  
 R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925  
 R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674  
 R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068  
 5 R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547  
 R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175  
 R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:AB018333  
 R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:U29091  
 10 R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064  
 R-nnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250  
 R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456  
 15 R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081  
 R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429  
 R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601  
 R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638  
 R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:AI309761  
 20 R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426  
 R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280  
 R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333  
 25 R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360  
 R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005  
 R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965  
 R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511  
 R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193  
 30 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485  
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587  
 R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
 35 R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415  
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
 R-THYRO1000637  
 R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H. sapiens]//4.9e-46:245:95//Hs.97398:AA398634  
 40 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
 R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384  
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063  
 45 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
 R-THYRO1000712  
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
 50 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624  
 R-THYRO1000777  
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
 55 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144  
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381  
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594  
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

R-THYRO1000829  
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627  
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881  
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011  
 5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663  
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871  
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234  
 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:  
 10 566:94//Hs.78106:AF079529  
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182  
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859  
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761  
 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.  
 15 14454:AF047440  
 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881  
 R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thal-  
 iana]//1.6e-90:474:93//Hs.106616:AI027524  
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777  
 20 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131  
 R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.  
 44049:AA521489  
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717  
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070  
 25 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223  
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497  
 R-THYRO1001100  
 R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//  
 6.6e-86:491:89//Hs.89135:AI138834  
 30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:  
 AJ006417  
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399  
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922  
 R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853  
 35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075  
 R-THYRO1001177  
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744  
 R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151  
 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932  
 40 R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629  
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640  
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561  
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269  
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230  
 45 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.  
 82314:M31642  
 R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250  
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033  
 50 R-THYRO1001365  
 R-THYRO1001374  
 R-THYRO001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:467:75//Hs.37181:D64108  
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627  
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733  
 55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197  
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979  
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.  
 159187:AB007977

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R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172  
R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082  
R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219  
5 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135  
R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110  
R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094  
10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936  
R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594  
R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413  
R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958  
15 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741  
R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247  
R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025  
R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886  
R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase (DHAPAT)  
20 mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190  
R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874  
R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282  
R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446  
R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//  
25 Hs.118633:AJ225089  
R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957  
R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726  
R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691  
30 R-THYRO1001721  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184  
R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172  
R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323  
R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474  
35 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224  
R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788  
R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956  
R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123  
40 R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314  
R-VESEN1000122  
R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289  
R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321  
45 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178  
R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540  
R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629  
R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792  
50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849  
R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991  
R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103  
R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812  
55 R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624  
R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936  
R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363  
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

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R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635  
 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210  
 R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808  
 5 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//  
 4.4e-66:339:97//Hs.8215:AA521150  
 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-  
 44:279:88//Hs.139007:H74314  
 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018  
 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613  
 10 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758  
 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292  
 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-  
 60:362:88//Hs.6381:AI188509  
 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320  
 15 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881  
 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.  
 41723:U37426  
 R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848  
 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:  
 20 AI125280  
 R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455  
 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:  
 AF060503  
 25 R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818  
 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:  
 95//Hs.83023:AF093670  
 R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III  
 [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330  
 30 R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405  
 R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463  
 R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433  
 R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359  
 R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512  
 35 R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642  
 R-nnnnnnnnnnnnnr//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405  
 R-Y79AA1000805  
 R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227  
 R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650  
 40 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.  
 55836:U85647  
 R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079  
 R-Y79AA1000968  
 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181  
 45 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049  
 R-Y79AA1000985  
 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851  
 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067  
 R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407  
 50 R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325  
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:  
 AB011135  
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047  
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260  
 55 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155  
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015  
 R-Y79AA1001167  
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884



R-Y79AA1001185  
 R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051  
 R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933  
 R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750  
 5 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674  
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and  
 IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892  
 R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271  
 R-Y79AA1001299//Human Ini1 mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847  
 10 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149  
 R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084  
 R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143  
 R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819  
 R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859  
 15 R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891  
 R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thal-  
 iana]/4.4e-109:553:95//Hs.106616:AI027524  
 R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704  
 R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]/6.2e-46:260:  
 20 94//Hs.24884:AA176812  
 R-nnnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563  
 R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872  
 R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177  
 R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508  
 25 R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237  
 R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204  
 R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]/7.2e-81:400:97//Hs.13323:AA897542  
 R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486  
 R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]/2.5e-19:112:97//Hs.26252:  
 30 AA643235  
 R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]/9.7e-99:553:92//Hs.  
 108896:R54040  
 R-nnnnnnnnnnnnn  
 R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783  
 35 R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490  
 R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for  
 a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phos-  
 phatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//  
 Hs.21864:AL031652  
 40 R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]/9.4e-87:427:97//Hs.18645:AI023798  
 R-nnnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809  
 R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]/8.1e-95:530:  
 91//Hs.72444:W23217  
 R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582  
 45 R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355  
 R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630  
 R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094  
 R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652  
 R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404  
 50 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275  
 R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135  
 R-Y79AA1002089//Homo sapiens PYRJN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080  
 R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933  
 R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785  
 55 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275  
 R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399  
 R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858  
 R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725

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R-nnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715  
R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]/3.5e-108:553:95//Hs.  
50441:AA747428  
R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349  
5 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]/  
6.5e-86:518:90//Hs.25682:AA857843  
R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274  
R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977  
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:  
10 AB014592  
R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]/9.0e-102:  
507:96//Hs.25895:AI341537  
R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555  
R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288  
15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:  
AB014534  
R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985  
R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371  
R-Y79AA1002361  
20 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908  
R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000  
R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026  
R-nnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]  
25 //4.4e-62:390:88//Hs.143930:AI207821  
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

## 30 Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
es. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be  
compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Ho-  
35 mology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash  
mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712  
C-HEMBA1000030  
40 C-HEMBA1000046  
C-HEMBA1000050  
C-HEMBA1000076  
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
1.9E-12//368aa//24%//P08553  
45 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584  
C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662  
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555  
C-HEMBA1000193  
C-HEMBA1000227  
50 C-HEMBA1000288  
C-HEMBA1000302  
C-HEMBA1000304  
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-  
49//107aa//91 %//O35594  
55 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//  
AL049654  
C-HEMBA1000387  
C-HEMBA1000392

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C-HEMBA1000460  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279  
 C-HEMBA1000501  
 5 C-HEMBA1000508  
 C-HEMBA1000520  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS).//2.6E-12//73aa//41%//P02826  
 C-HEMBA1000534  
 10 C-HEMBA1000555  
 C-HEMBA1000568  
 C-HEMBA1000588  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295  
 C-HEMBA1000636  
 15 C-HEMBA1000682  
 C-HEMBA1000686  
 C-HEMBA1000719  
 C-HEMBA1000727  
 C-HEMBA1000752  
 20 C-HEMBA1000817  
 C-HEMBA1000851  
 C-HEMBA1000867  
 C-HEMBA1000869  
 C-HEMBA1000872  
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//  
 1.6E-30//127aa//40%//P43366  
 C-HEMBA1000918  
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-  
 MOSOME X.//1E-10//288aa//23%//Q19124  
 30 C-HEMBA1000946  
 C-HEMBA1000968  
 C-HEMBA1000971  
 C-HEMBA1000975  
 C-HEMBA1001009  
 35 C-HEMBA1001022  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//  
 1.4E-12//131aa//38%//Q01485  
 C-HEMBA1001052  
 C-HEMBA1001080  
 40 C-HEMBA1001085  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//  
 176aa//57%//P48059  
 C-HEMBA1001109  
 C-HEMBA1001122  
 45 C-HEMBA1001133  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)  
 (FRAGMENT).//1.5E-116//197aa//58%//Q06730  
 C-HEMBA1001140  
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646  
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//  
 AB020678  
 C-HEMBA1001235  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733  
 C-HEMBA1001281  
 55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//  
 29%//Q60401  
 C-HEMBA1001303  
 C-HEMBA1001310

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C-HEMBA1001326  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081  
 5 C-HEMBA1001388  
 C-HEMBA1001398  
 C-HEMBA1001405  
 C-HEMBA1001407  
 C-HEMBA1001413  
 10 C-HEMBA1001415  
 C-HEMBA1001446  
 C-HEMBA1001450  
 C-HEMBA1001455  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850  
 15 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166  
 C-HEMBA1001533  
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657  
 C-HEMBA1001581  
 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450  
 25 C-HEMBA1001702  
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386  
 C-HEMBA1001731  
 C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009  
 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675  
 C-HEMBA1001815  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676  
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230  
 C-HEMBA1001864  
 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342  
 C-HEMBA1001987  
 C-HEMBA1002018  
 40 C-HEMBA1002049  
 C-HEMBA1002084  
 C-HEMBA1002125  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293  
 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694  
 C-HEMBA1002191  
 C-HEMBA1002199  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161  
 50 C-HEMBA1002237  
 C-HEMBA1002265  
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537  
 C-HEMBA1002349  
 55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563  
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793  
 C-HEMBA1002430

C-HEMBA1002439  
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994  
 C-HEMBA1002460  
 C-HEMBA1002462  
 5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175  
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%//P17437  
 C-HEMBA1002477  
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732  
 10 C-HEMBA1002515  
 C-HEMBA1002542  
 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%//AF075587  
 C-HEMBA1002583  
 15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169  
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351  
 C-HEMBA1002688  
 C-HEMBA1002696  
 C-HEMBA1002750  
 20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414  
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636  
 C-HEMBA1002777  
 C-HEMBA1002794  
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185  
 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1002850  
 C-HEMBA1002863  
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%//Q09297  
 30 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148  
 C-HEMBA1002937  
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//P16157  
 35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710  
 C-HEMBA1002954  
 C-HEMBA1002971  
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646  
 40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//5 34aa//24%//Q02224  
 C-HEMBA1003033  
 C-HEMBA1003035  
 C-HEMBA1003041  
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439  
 45 C-HEMBA1003067  
 C-HEMBA1003096  
 C-HEMBA1003117  
 C-HEMBA1003129  
 50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940  
 C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%//AL079278  
 55 C-HEMBA1003175  
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551  
 C-HEMBA1003199

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C-HEMBA1003222  
 C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%//Q02088  
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%//Q06548  
 C-HEMBA1003257  
 5 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%//P32506  
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//  
 1043bp//99%//AB024436  
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%//AB011109  
 C-HEMBA1003322  
 10 C-HEMBA1003327  
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.00000002//248aa//23%//Q02224  
 C-HEMBA1003370  
 C-HEMBA1003380  
 C-HEMBA1003395  
 15 C-HEMBA1003402  
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%//AB020712  
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6e-312//  
 1414bp//99%//AL050287  
 C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709  
 20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139  
 C-HEMBA1003447  
 C-HEMBA1003461  
 C-HEMBA1003463  
 C-HEMBA1003528  
 25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%//P50480  
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//P53384  
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-  
 MA-I).//1.2E-31//71aa//100%//P16874  
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-  
 30 49//279aa//32%//P19474  
 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%//Q13330  
 C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039  
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//  
 35 35%//P19682  
 C-HEMBA1003615  
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%//AB015344  
 C-HEMBA1003621  
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q13207  
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973  
 40 C-HEMBA1003711  
 C-HEMBA1003807  
 C-HEMBA1003864  
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//  
 89aa//46%//P16372  
 45 C-HEMBA1003959  
 C-HEMBA1003989  
 C-HEMBA1004074  
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%//  
 AF091234  
 50 C-HEMBA1004146  
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%//AB023145  
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748  
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%//  
 AF095927  
 55 C-HEMBA1004246  
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//  
 99%//AF092094  
 C-HEMBA1004289

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C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955  
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//  
 AF089841  
 C-HEMBA1004596  
 5 C-HEMBA1004693  
 C-HEMBA1004736  
 C-HEMBA1004753  
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082  
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//  
 10 L39060  
 C-HEMBA1004763  
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547  
 C-HEMBA1004771  
 C-HEMBA1004776  
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851  
 C-HEMBA1004806  
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//  
 Q00004  
 C-HEMBA1004850  
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//  
 100%//AL080114  
 C-HEMBA1004923  
 C-HEMBA1004929  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401  
 25 C-HEMBA1004933  
 C-HEMBA1004954  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
 0.00000096//286aa//23%//P12036  
 C-HEMBA1005475  
 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270  
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//  
 151aa//37%//P16372  
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-  
 225//1189bp//88%//AF076183  
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043  
 C-HEMBA1006377  
 C-HEMBA1006467  
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552  
 C-HEMBA1006530  
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 0.000000043//111aa//40%//Q01485  
 C-HEMBA1006795  
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258  
 C-HEMBA1006936  
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//  
 AP078849  
 C-HEMBA1007342  
 C-HEMBA1000008  
 C-HEMBA1000018  
 50 C-HEMBA1000024  
 C-HEMBA1000025  
 C-HEMBA1000036  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//  
 1582bp//80%//AF084928  
 55 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799  
 C-HEMBA1000103  
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEMBB1000136  
 C-HEMBB1000215  
 C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5//  
 2.7E-12//112aa//47%//Q09530  
 5 C-HEMBB1000244  
 C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-  
 MOSOME V.//6.1E-09//242aa//26%//Q23256  
 C-HEMBB1000338  
 C-HEMBB1000339  
 10 C-HEMBB1000391  
 C-HEMBB1000438  
 C-HEMBB1000449  
 C-HEMBB1000589  
 C-HEMBB1000591  
 15 C-HEMBB1000623  
 C-HEMBB1000630  
 C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//  
 232aa//28%//P78970  
 C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671  
 20 C-HEMBB1000671  
 C-HEMBB1000673  
 C-HEMBB1000705  
 C-HEMBB1000706  
 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//  
 25 U53475  
 C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847  
 C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//  
 1.2E-126//613bp//97%//AF111105  
 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-  
 30 54//232aa//43%//P39956  
 C-HEMBB1000807  
 C-HEMBB1000810  
 C-HEMBB1000848  
 C-HEMBB1000852  
 35 C-HEMBB1000870  
 C-HEMBB1000887  
 C-HEMBB1000908  
 C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102  
 C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//  
 40 99%//AF116910  
 C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974  
 C-HEMBB1000975  
 C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-  
 18//178aa//30%//P28575  
 45 C-HEMBB1000991  
 C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//  
 P51523  
 C-HEMBB1001014  
 C-HEMBB1001024  
 50 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087  
 C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//  
 80%//AF010144  
 C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803  
 55 C-HEMBB1001096  
 C-HEMBB1001105  
 C-HEMBB1001117  
 C-HEMBB1001126



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C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-  
 210//1835bp//76%//AF110267  
 C-HEMBB1001153  
 5 C-HEMBB1001169  
 C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357  
 C-HEMBB1001182  
 C-HEMBB1001199  
 C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187  
 10 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-  
 284//713bp//100%//AF089897  
 C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966  
 C-HEMBB1001289  
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081  
 15 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//  
 724bp//86%//U92703  
 C-HEMBB1001331  
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175  
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mi-  
 20 tochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441  
 C-HEMBB1001369  
 C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001387  
 C-MAMMA1002317  
 25 C-MAMMA1002319  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926  
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190  
 C-NT2RM1000242  
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028  
 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-  
 PASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942  
 C-NT2RM1000669  
 C-NT2RM1000781  
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138  
 35 C-NT2RM1001008  
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360  
 C-NT2RM1001074  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//  
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseu-  
 40 dogene similar to MMS2, ESTs and GSSs, complete sequence.//0//1740bp//99%//AL031291  
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167  
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTER-  
 MEDIATE CHAIN).//0.00000043//136aa//31%//P54703  
 45 C-NT2RM2000032  
 C-NT2RM2000042  
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//  
 1.3E-36//160aa//40%//P50102  
 50 C-NT2RM2000093  
 C-NT2RM2000101  
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//  
 99%//AF067223  
 C-NT2RM2000192  
 55 C-NT2RM2000239  
 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2E-314//  
 1416bp//100%//AL080069  
 C-NT2RM2000259

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C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//  
P14918  
C-NT2RM2000287  
5 C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//  
AB020666  
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132  
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274  
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//  
U48251  
10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-  
OTIDE//1.7E-68//419aa//36%//P50849  
C-NT2RM2000374  
C-NT2RM2000395  
15 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-  
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
NENT).//1.6E-54//344aa//33%//P32802  
C-NT2RM2000407  
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//  
Q08469  
20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//  
157aa//28%//P36113  
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%//  
P22211  
25 C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823  
C-NT2RM2000502  
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243  
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//  
32%//P17437  
30 C-NT2RM2000540  
C-NT2RM2000567  
C-NT2RM2000569  
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
1.7E-187//741aa//46%//P73505  
35 C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987  
C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973  
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//  
0//2712bp//99%//AF156487  
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//  
AF179221  
40 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
SRP75).//4.4E-32//319aa//35%//Q08170  
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272  
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558  
C-NT2RM2000639  
45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576  
C-NT2RM2000669  
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391  
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//  
36%//Q15404  
50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342  
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//  
P41877  
C-NT2RM2000795  
55 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//  
98%//P23514  
C-NT2RM2000837  
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//  
AB015046

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C-NT2RM2000952  
C-NT2RM2000984  
C-NT2RM2001004  
5 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809  
C-NT2RM2001065  
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//  
26%//P46577  
C-NT2RM2001131  
C-NT2RM2001141  
10 C-NT2RM2001152  
C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//  
1335bp//99%//AL080109  
C-NT2RM2001194  
C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143  
15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//  
P48724  
C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//  
32%//P97924  
C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
20 DOHYDROLASE).//1.3E-180//328aa//99%//P13264  
C-NT2RM2001243  
C-NT2RM2001247  
C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//  
P53995  
25 C-NT2RM2001291  
C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//  
AL080063  
C-NT2RM2001312  
C-NT2RM2001319  
30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584  
C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808  
C-NT2RM2001370  
C-NT2RM2001393  
C-NT2RM2001420  
35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//  
100%//AL050146  
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//  
437aa//57%//P52569  
C-NT2RM2001504  
40 C-NT2RM2001524  
C-NT2RM2001544  
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//  
90aa//42%//P38660  
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-  
45 61//312aa//44%//P19474  
C-NT2RM2001582  
C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610  
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692  
C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931  
50 C-NT2RM2001930  
C-NT2RM2001935  
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320  
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//  
212aa//23%//P38250  
55 C-NT2RM2001982  
C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//  
P37838  
C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%/Q12730  
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//  
 30%/Q09782  
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
 5 0.000000029//83aa//44%/P40796  
 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//  
 425aa//41%/P46837  
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//  
 0//1959bp//99%/AB016789  
 10 C-NT2RM2002049  
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//  
 24%/Q07878  
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
 5E-62//104aa//57%/Q61990  
 15 C-NT2RM2002091  
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840  
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//  
 1868bp//99%/AF030435  
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//  
 20 26%/P49695  
 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805  
 C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//  
 99%/AL117402  
 25 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167  
 C-NT2RM4000061  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%/X68101  
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%/P25386  
 30 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381  
 C-NT2RM4000197  
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255  
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//  
 35 633bp//64%/L20303  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//  
 97%/M99438  
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637  
 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%/Q24371  
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%/AB025412  
 C-NT2RM4000395  
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769  
 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//  
 24%/Q10297  
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%/AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-  
 TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%/P04280  
 50 C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955  
 C-NT2RM4000511  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)  
 (FRAGMENT).//1.1E-11//394aa//24%/P16884  
 C-NT2RM4000520  
 55 C-NT2RM4000585  
 C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//  
 1.1E-285//1293bp//99%/AF186273  
 C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587

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C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000040  
 C-NT2RP1000063  
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834  
 5 C-NT2RP1000101  
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471  
 C-NT2RP1000112  
 C-NT2RP1000124  
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859  
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165  
 C-NT2RP1000170  
 C-NT2RP1000191  
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357  
 C-NT2RP1000243  
 15 C-NT2RP1000259  
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730  
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551  
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447  
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343  
 C-NT2RP1000357  
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187  
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159  
 C-NT2RP1000416  
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423  
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257  
 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580  
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653  
 C-NT2RP1000481  
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686  
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020  
 C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367  
 40 C-NT2RP1000581  
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233  
 C-NT2RP1000688  
 C-NT2RP1000695  
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379  
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434  
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//Q35566  
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960  
 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223  
 C-NT2RP1000846  
 C-NT2RP1000851  
 55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//Q35566  
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823  
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-

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105//504bp//99%//U39317  
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652  
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823  
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//  
 5 M17885  
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338  
 C-NT2RP1000980  
 C-NT2RP1000988  
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//  
 10 1529bp//61%//L01790  
 C-NT2RP1001014  
 C-NT2RP1001395  
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917  
 C-NT2RP1001424  
 15 C-NT2RP1001449  
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//  
 100%//AJ005257  
 C-NT2RP1001466  
 C-NT2RP1001475  
 20 C-NT2RP1001482  
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891  
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//  
 P42803  
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 25 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//O35566  
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//  
 271aa//89%//P47758  
 C-NT2RP1001616  
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594  
 30 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//  
 55%//O34136  
 C-NT2RP2000007  
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//  
 P51523  
 35 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//  
 34%//Q01730  
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 0//1390bp//98%//AF061749  
 C-NT2RP2000054  
 40 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-  
 SILON).//9.4E-16//45aa//100%//P49446  
 C-NT2RP2000067  
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//  
 383aa//32%//P33450  
 45 C-NT2RP2000079  
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338  
 C-NT2RP2000091  
 C-NT2RP2000097  
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356  
 50 C-NT2RP2000120  
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//  
 P41877  
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206  
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN  
 55 AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585  
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891  
 C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

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C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//  
 AB023225  
 C-NT2RP2000173  
 C-NT2RP2000175  
 5 C-NT2RP2000195  
 C-NT2RP2000205  
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568  
 C-NT2RP2000232  
 10 C-NT2RP2000233  
 C-NT2RP2000239  
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558  
 C-NT2RP2000270  
 15 C-NT2RP2000274  
 C-NT2RP2000283  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//  
 25%//Q10297  
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676  
 20 C-NT2RP2000298  
 C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//  
 1193bp//99%//U82381  
 C-NT2RP2000328  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 25 226aa//92%//P08760  
 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//  
 674aa//46%//P17564  
 C-NT2RP2000369  
 C-NT2RP2000412  
 30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//  
 100%//P52597  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//  
 99%//AF102265  
 C-NT2RP2000438  
 35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844  
 C-NT2RP2000503  
 C-NT2RP2000510  
 C-NT2RP2000516  
 C-NT2RP2000603  
 40 C-NT2RP2000617  
 C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514  
 C-NT2RP2000656  
 C-NT2RP2000658  
 C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 45 C-NT2RP2000704  
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.7E-100//  
 488aa//44%//O32038  
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623  
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680  
 50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//  
 29%//Q99104  
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//  
 P13466  
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174  
 55 C-NT2RP2000819  
 C-NT2RP2000841  
 C-NT2RP2000845  
 C-NT2RP2000863

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C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/060841  
 C-NT2RP2000892  
 C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244  
 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%/AL050390  
 5 C-NT2RP2000938  
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%/AB018298  
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704  
 C-NT2RP2000985  
 10 C-NT2RP2001036  
 C-NT2RP2001044  
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%/AB007957  
 C-NT2RP2001065  
 15 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.8E-46//222aa//45%/Q20939  
 C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232  
 C-NT2RP2001094  
 C-NT2RP2001119  
 20 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440  
 C-NT2RP2001218  
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.2E-10//366aa//28%/P14105  
 C-NT2RP2001381  
 25 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp//100%/AL080146  
 C-NT2RP2001427  
 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%/AB018340  
 C-NT2RP2001675  
 30 C-NT2RP2001721  
 C-NT2RP2001907  
 C-NT2RP2001969  
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378  
 35 C-NT2RP2002046  
 C-NT2RP2002154  
 C-NT2RP2002208  
 C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%/P42568  
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521  
 40 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%/AB015594  
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958  
 C-NT2RP2002426  
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289  
 45 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073  
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815  
 50 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345  
 C-NT2RP2002621  
 C-NT2RP2002672  
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%/O14345  
 55 C-NT2RP2002769  
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764



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C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392

C-NT2RP2002954

5 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669

C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129

C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190

C-NT2RP2003108

10 C-NT2RP2003117

C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//AF079765

C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652

C-NT2RP2003177

15 C-NT2RP2003194

C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811

C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572

C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337

20 C-NT2RP2003367

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378

C-NT2RP2003446

C-NT2RP2003533

25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261

C-NT2RP2003596

C-NT2RP2003629

C-NT2RP2003687

30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669

C-NT2RP2003793

35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175

C-NT2RP2003986

C-NT2RP2004042

C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820

40 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120

C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044

C-NT2RP2004463

45 C-NT2RP2004602

C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291

C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%//Q92355

50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490

C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588

C-NT2RP2004802

55 C-NT2RP2004841

C-NT2RP2004936

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692

C-NT2RP2004999

C-NT2RP2005000  
 C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515  
 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779  
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447  
 5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743  
 C-NT2RP2005140  
 C-NT2RP2005147  
 C-NT2RP2005159  
 10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025  
 C-NT2RP2005270  
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053  
 C-NT2RP2005293  
 C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576  
 15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247  
 C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823  
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170  
 20 C-NT2RP2005441  
 C-NT2RP2005453  
 C-NT2RP2005464  
 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127  
 C-NT2RP2005472  
 25 C-NT2RP2005495  
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876  
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803  
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563  
 30 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526  
 C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963  
 C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366  
 35 C-NT2RP2005555  
 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529  
 C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085  
 40 C-NT2RP2005622  
 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623  
 C-NT2RP2005637  
 C-NT2RP2005640  
 45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101  
 C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973  
 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814  
 C-NT2RP2005683  
 50 C-NT2RP2005690  
 C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342  
 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.000000003//169aa//28%//P38074  
 C-NT2RP2005748  
 55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868  
 C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

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C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)//1.7E-61//374aa//38%//P47943  
 C-NT2RP2005767//G.gallus PB1 gene//5E-163//1158bp//81%//X90849  
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//  
 2.7E-180//656bp//99%//AF151351  
 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-  
 CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-  
 BINDING PROTEIN) (SABP)//2.1E-213//249aa//85%//Q02038  
 C-NT2RP2005781  
 C-NT2RP2005804  
 10 C-NT2RP2005835//SHP1 PROTEIN//1.8E-28//208aa//32%//P34223  
 C-NT2RP2005853  
 C-NT2RP2005868  
 C-NT2RP2005886  
 C-NT2RP2005890  
 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188  
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57)//5E-11//155aa//34%//P48837  
 C-NT2RP2006038  
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75)//1.5E-13//185aa//38%//Q08170  
 20 C-NT2RP2006052  
 C-NT2RP2006069  
 C-NT2RP2006071  
 C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102)//0//1759bp//  
 99%//AL049970  
 25 C-NT2RP2006106  
 C-NT2RP2006141  
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554  
 C-NT2RP2006196  
 C-NT2RP2006200  
 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484  
 C-NT2RP2006237  
 C-NT2RP2006238  
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1]//2E-59//  
 388aa//32%//P46821  
 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262  
 C-NT2RP2006333  
 C-NT2RP2006365  
 C-NT2RP2006393  
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX)//  
 40 0.00000034//50aa//50%//Q61658  
 C-NT2RP2006456  
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266  
 C-NT2RP2006467  
 C-NT2RP2006472  
 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710  
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE)//4.2E-134//  
 486aa//50%//P24461  
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP)//0.0000055//  
 169aa//25%//P09543  
 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708  
 C-NT2RP3000072  
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164  
 C-NT2RP3000220  
 C-NT2RP3000251  
 55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334  
 C-NT2RP3000312  
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor  
 Sp1.//0//1544bp//100%//AJ242978

C-NT2RP3000333  
 C-NT2RP3000348  
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN  
 HP0303.//0.00000028//185aa//31%//O25074  
 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 226aa//92%//P08760  
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1  
 and Prp6.//0//2072bp//98%//AB019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293  
 10 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//  
 1.7E-139//679aa//41%//O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
 C-NT2RP3000484  
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160  
 15 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//  
 P15151  
 C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283  
 C-NT2RP3000599  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523  
 20 C-NT2RP3000644  
 C-NT2RP3000661  
 C-NT2RP3000665  
 C-NT2RP3000690  
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650  
 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//Q61982  
 C-NT2RP3000836  
 C-NT2RP3000841  
 C-NT2RP3000850  
 C-NT2RP3000852  
 30 C-NT2RP3000859  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds.//6.9E-69//1611bp//61%//U53445  
 C-NT2RP3000869  
 C-NT2RP3000901  
 35 C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%//AF064257  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 2.7E-185//585bp//88%//AF015264  
 C-NT2RP3000980  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN  
 40 STAUFEN.//0.00000006//78aa//48%//P25159  
 C-NT2RP3001004  
 C-NT2RP3001081  
 C-NT2RP3001084  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433  
 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201  
 C-NT2RP3001109  
 C-NT2RP3001116  
 C-NT2RP3001119  
 C-NT2RP3001133  
 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//  
 196aa//27%//P53154  
 C-NT2RP3001214  
 55 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//  
 P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-  
 BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

C-NT2RP3001236  
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1]//1.2E-166//395aa//51%//P14873  
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718  
 5 C-NT2RP3001307  
 C-NT2RP3001325  
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905  
 C-NT2RP3001392  
 10 C-NT2RP3001396  
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF//1.3E-61//374aa//36%//P49711  
 C-NT2RP3001407//SCY1 PROTEIN//0.00000033//143aa//25%//P53009  
 C-NT2RP3001420  
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT)//1E-16//77aa//46%//O33529  
 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG//2.7E-10//159aa//33%//O09053  
 C-NT2RP3001457  
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//9.1E-13//87aa//43%//P11632  
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395  
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801  
 20 C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN//1E-61//345aa//42%//P20964  
 C-NT2RP3001621  
 C-NT2RP3001629  
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210//6.8E-18//91aa//38%//Q92609  
 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2//8.8E-09//132aa//31%//O22468  
 C-NT2RP3001676  
 C-NT2RP3001679  
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE//1.6E-11//348aa//27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)//7.4E-18//249aa//30%//Q04652  
 30 C-NT2RP3001896  
 C-NT2RP3001915  
 C-NT2RP3001929  
 C-NT2RP3003193//ZINC FINGER PROTEIN 135//7.3E-98//269aa//62%//P52742  
 C-NT2RP3004466  
 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.3E-113//466aa//42%//P34110  
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532  
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126  
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)//0.000000038//150aa//28%//Q01484  
 40 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445  
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946  
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266  
 45 C-NT2RP3004617//ZINC-BINDING PROTEIN A33//7.2E-75//464aa//35%//Q02084  
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097  
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)//1.7E-72//254aa//45%//P54352  
 50 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64//2.6E-98//239aa//64%//P35526  
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65//4.9E-51//335aa//37%//Q64375  
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657  
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538  
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//0//728aa//99%//Q10568  
 55 C-NT2RP4000129  
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150  
 C-NT2RP4000151  
 C-NT2RP4000159  
 C-NT2RP4000185  
 5 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600  
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//  
 P15287  
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470  
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173  
 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968  
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.5E-297//1024aa//  
 55%//P87115  
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
 SE).//1.5E-26//237aa//28%//Q01631  
 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//  
 32%//P26372  
 C-NT2RP4000355  
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281  
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//  
 20 4782bp//99%//AF044195  
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-  
 77//262aa//54%//O75570  
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
 C-NT2RP4000381  
 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738  
 C-NT2RP4000415  
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-AL-  
 PHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701  
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//  
 30 99%//AL050078  
 C-NT2RP4000449  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//  
 35 2.5E-37//291aa//38%//P50101  
 C-NT2RP4000480  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//  
 1.9E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484  
 40 C-NT2RP4000500  
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818  
 C-NT2RP4000524  
 C-NT2RP4000541  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319  
 45 C-NT2RP4000560  
 C-NT2RP4000588  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//  
 99%//AF067730  
 C-NT2RP4000638  
 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//  
 30%//P39625  
 C-NT2RP4000704  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//  
 55 Q11073  
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267  
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148  
 C-NT2RP4000737

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C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229  
C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
0.000000032//67aa//31%//P53915  
5 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939  
C-NT2RP4000833  
C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265  
C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808  
C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-  
NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175  
10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415  
C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682  
C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314  
C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//  
227aa//36%//Q06828  
15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//1.5E-76//346aa//43%//Q61068  
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900  
20 C-NT2RP4000955  
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//  
90aa//42%//P38660  
C-NT2RP4000975  
C-NT2RP4000979  
25 C-NT2RP4000984  
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579  
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968  
30 C-NT2RP4001006  
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181  
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.5E-  
92//443aa//44%//Q09996  
C-NT2RP4001057  
35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375  
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE)//1.3E-123//  
563aa//46%//P13586  
C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967  
C-NT2RP4001086  
40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-  
INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400  
C-NT2RP4001100  
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//  
P38378  
45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736  
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283  
C-NT2RP4001138  
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP).//0.00000021//  
93aa//33%//P44514  
50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750  
C-NT2RP4001149  
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
3.4E-29//385aa//29%//P35331  
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
55 4.7E-29//227aa//35%//P52178  
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//  
65 %//U95760  
C-NT2RP4001207

C-NT2RP4001210  
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//  
 90aa//42%/P38660  
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%/Q04652  
 5 C-NT2RP4001235  
 C-NT2RP4001256  
 C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%/AB020682  
 C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%/U49082  
 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32-%/Q07283  
 10 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-  
 CASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/P24391  
 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119  
 C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein.//9.2E-160//736bp//99%/AJ007014  
 15 C-NT2RP4001343  
 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//  
 1400bp//100%/AB017494  
 C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds.//1.4E-58//2425bp//59%/U53445  
 20 C-NT2RP4001353  
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-  
 19//222aa//30%/Q08180  
 C-NT2RP4001373  
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 25 TEIN KINASE 1).//9.2E-17//146aa//35%/P18160  
 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1.//2E-53//436aa//30%/Q10085  
 C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%/AB023140  
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%/Q14141  
 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%/Q99676  
 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131  
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-  
 PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218  
 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010  
 C-NT2RP4001502  
 C-NT2RP4001507  
 C-NT2RP4001524  
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-  
 40 54//242aa//3 8%/P25656  
 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//3202bp//99%/AF152961  
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%/P96902  
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26,%/Q02453  
 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197  
 C-NT2RP4001571  
 C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756  
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%/AJ223830  
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//  
 50 1.7E-141//373aa//47%/P73505  
 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676  
 C-NT2RP4001614  
 C-NT2RP4001634  
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%/P40469  
 55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323  
 C-NT2RP4001677  
 C-NT2RP4001679  
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF



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100 KD SUBUNIT).//4E-10//243aa//25%/Q10568  
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%/Q10282  
 5 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332  
 C-NT2RP4001739  
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%/P51523  
 10 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174  
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%/AB023232  
 C-NT2RP4001803  
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/O35566  
 15 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%/P55083  
 C-NT2RP4001828  
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%/AF155595  
 C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%/P37709  
 20 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%/AL050390  
 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aa//25%/Q00808  
 C-NT2RP4001901  
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%/Q12024  
 25 C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%/P49711  
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%/Q43209  
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%/P13816  
 30 C-NT2RP4001953  
 C-NT2RP4001966  
 C-NT2RP4001975  
 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%/Q04652  
 C-NT2RP4002052  
 35 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1E-137//679aa//40%/O43143  
 C-NT2RP4002071  
 C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//39%/Q05481  
 40 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%/P52655  
 C-NT2RP4002298  
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%/P38938  
 C-NT2RP4002791  
 45 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434FI 72 (from clone DKFZp434F172).//0//2557bp//99%/AL080202  
 C-NT2RP4002905  
 C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552  
 C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%/Q00808  
 50 C-NT2RP5003492  
 C-NT2RP5003500  
 C-NT2RP5003506  
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%/P37116  
 55 C-NT2RP5003524  
 C-NT2RP5003534  
 C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262  
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%/

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O14727  
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922  
C-OVARC1000035  
5 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE)//  
0.0000032//60aa//45 %//P80022  
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874  
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)//  
8.4E-14//259aa//30%//P51610  
C-OVARC1000113  
10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955  
C-OVARC1000148  
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//  
2.5E-95//461bp//98%//AJ242975  
C-OVARC1000168  
15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//  
AF068332  
C-OVARC1000212  
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
(MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665  
20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-  
CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//  
30%//P14904  
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249  
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363  
25 C-OVARC1000321  
C-OVARC1000326  
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//  
200aa//27%//P40004  
C-OVARC1000347  
30 C-OVARC1000384  
C-OVARC1000411  
C-OVARC1000420  
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205  
C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//  
35 99%//AL080126  
C-OVARC1000461  
C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075  
C-OVARC1000466  
C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452  
C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636  
C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850  
C-OVARC1000564  
C-OVARC1000576  
45 C-OVARC1000588  
C-OVARC1000605  
C-OVARC1000640  
C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
plete cds.//0//1812bp//98%//D43772  
50 C-OVARC1000661  
C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886  
C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343  
C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533  
C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//01//1172bp//97%//AJ130978  
55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946  
C-OVARC1001162  
C-OVARC1001243  
C-OVARC1001296

C-OVARC1001360  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//  
 99%//AJ224819  
 C-OVARC1001425  
 5 C-PLACE1000005  
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//  
 134aa//43%//P52046  
 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%//  
 10 AB020639  
 C-PLACE1000185  
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194  
 C-PLACE1000347  
 C-PLACE1000374  
 15 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660  
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//  
 P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246  
 20 C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//  
 0.0000028//134aa//29%//P53368  
 C-PLACE1000435  
 C-PLACE1000444  
 C-PLACE1000562  
 25 C-PLACE1000564  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-  
 BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455  
 C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//  
 30 AF044201  
 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891  
 C-PLACE1000716  
 C-PLACE1000748  
 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449  
 35 C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548  
 C-PLACE1000798  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN  
 YHR148W.//2.5E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010  
 40 C-PLACE1000948  
 C-PLACE1000972  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070  
 C-PLACE1001000  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
 45 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652  
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-  
 UIEM).//3E-33//138aa//42%//Q61103  
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//  
 132aa//46%//Q12929  
 50 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0//2118bp//  
 99%//AC005412  
 C-PLACE1001412  
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered  
 pieces.//0//1440bp//99%//AL031660  
 55 C-PLACE1001503  
 C-PLACE1001570  
 C-PLACE1001610  
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

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(THIOESTERASE n).//4E-81//263aa//56%//P08635  
 C-PLACE1001729  
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381  
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//  
 5 Q57290  
 C-PLACE1001810  
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//  
 0//1995bp//99%//AF058953  
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524  
 10 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737  
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935  
 C-PLACE1001928  
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091  
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211  
 15 C-PLACE1002072  
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
 SE).//0.0000053//188aa//29%//P49606  
 C-PLACE1002140  
 C-PLACE1002163  
 20 C-PLACE1002170  
 C-PLACE1002433  
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105  
 C-PLACE1002465  
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256  
 25 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//  
 1750bp//99%//AF068180  
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391  
 C-PLACE1002794  
 C-PLACE1002815  
 30 C-PLACE1002839  
 C-PLACE1002851  
 C-PLACE1002941  
 C-PLACE1002996  
 C-PLACE1003045  
 35 C-PLACE1003092  
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268  
 C-PLACE1003108  
 C-PLACE1003145  
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 40 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743  
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750  
 C-PLACE1003200  
 C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//  
 99%//AL080133  
 45 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//  
 P51522  
 C-PLACE1003334  
 C-PLACE1003342  
 C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 50 cds.//0//2435bp//99%//U92715  
 C-PLACE1003369  
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200  
 C-PLACE1003611  
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824  
 55 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//8E-19//209aa//34%//Q08170  
 C-PLACE1003711  
 C-PLACE1003723

C-PLACE1003762  
 C-PLACE1003771  
 C-PLACE1003784  
 C-PLACE1003923  
 5 C-PLACE1003936  
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 2.4E-124//326aa//73%//P80385  
 C-PLACE1004104  
 C-PLACE1004114  
 10 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//6.1E-181//340aa//96%//P29387  
 C-PLACE1004149  
 C-PLACE1004156  
 C-PLACE1004161  
 15 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q62556  
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//  
 0//1882bp//99%//AF069493  
 C-PLACE1004258  
 20 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%//O15393  
 C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//  
 AF084830  
 C-PLACE1004289  
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750  
 25 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588  
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//  
 2512bp//99%//AF100153  
 C-PLACE1004376  
 C-PLACE1004388  
 30 C-PLACE1004405  
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%//Q63448  
 C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283  
 C-PLACE1004451  
 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823  
 C-PLACE1004473  
 C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//  
 99%//AF026445  
 C-PLACE1004516  
 40 C-PLACE1004548  
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100  
 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568  
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438  
 C-PLACE1004645  
 45 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%//  
 X66277  
 C-PLACE1004664  
 C-PLACE1004672  
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//  
 50 96%//P12815  
 C-PLACE1004691  
 C-PLACE1004722  
 C-PLACE1004736  
 C-PLACE1004740  
 55 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPO-  
 NENT) (N- RECOGNIN).//4.4E-35//578aa//27%//O60152  
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224//  
 790bp//98%//AB022918

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C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337  
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.7E-65//695aa//29%//Q01631  
 5 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170  
 C-PLACE1004824  
 C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891  
 C-PLACE1004885  
 10 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//O42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936  
 15 C-PLACE1004934  
 C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794  
 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073  
 C-PLACE1004982  
 20 C-PLACE1005026  
 C-PLACE1005027  
 C-PLACE1005046  
 C-PLACE1005077  
 C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401  
 25 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652  
 C-PLACE1005111  
 C-PLACE1005181  
 C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636  
 C-PLACE1005206  
 30 C-PLACE1005232  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 C-PLACE1005261  
 C-PLACE1005266  
 C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182  
 35 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352  
 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760  
 C-PLACE1005308  
 C-PLACE1005313  
 40 C-PLACE1005327  
 C-PLACE1005335  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//O33335  
 45 C-PLACE1005374  
 C-PLACE1005480  
 C-PLACE1005481  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276  
 50 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251  
 C-PLACE1005550  
 C-PLACE1005554  
 C-PLACE1005623  
 55 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

C-PLACE1005730  
 C-PLACE1005755  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
 (THIOESTERASE II).//2.5E-79//209aa//53%//P08635  
 5 C-PLACE1005803  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//  
 AF027156  
 C-PLACE1005851  
 C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120  
 10 C-PLACE1005923  
 C-PLACE1005925  
 C-PLACE1005934  
 C-PLACE1005936  
 C-PLACE1005951  
 15 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-  
 54//455aa//32%//P14904  
 C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//  
 25 254aa//25%//P38129  
 C-PLACE1005990  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876  
 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//  
 AF039023  
 25 C-PLACE1006139  
 C-PLACE1006159  
 C-PLACE1006167  
 C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706  
 C-PLACE1006195  
 30 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747  
 C-PLACE1006225  
 C-PLACE1006236  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//  
 P28675  
 35 C-PLACE1006246  
 C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//  
 1271-bp//99%//AL080066  
 C-PLACE1006335  
 C-PLACE1006357  
 40 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085  
 C-PLACE1006412  
 C-PLACE1006414  
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910  
 C-PLACE1006445  
 45 C-PLACE1006470  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595  
 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//  
 Q00004  
 C-PLACE1006492  
 50 C-PLACE1006531  
 C-PLACE1006552  
 C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
 2182bp//99%//AC007383  
 C-PLACE1006615  
 55 C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145  
 C-PLACE1006673  
 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//  
 734bp//62%//AB015630

C-PLACE1006704  
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263  
 C-PLACE1006782  
 5 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%//P08547  
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123  
 C-PLACE1006883  
 10 C-PLACE1006901  
 C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181  
 C-PLACE1006932  
 C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000  
 15 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998  
 C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421  
 C-PLACE1006961  
 C-PLACE1006962  
 20 C-PLACE1006966  
 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542  
 C-PLACE1007021  
 C-PLACE1007105  
 25 C-PLACE1007178  
 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%//P54304  
 C-PLACE1007238  
 C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%//D50495  
 30 C-PLACE1007242  
 C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579  
 C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908  
 C-PLACE1007274  
 35 C-PLACE1007282  
 C-PLACE1007301  
 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649  
 C-PLACE1007342  
 40 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870  
 C-PLACE1007367  
 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715  
 45 C-PLACE1007386  
 C-PLACE1007402  
 C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320  
 C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487  
 50 C-PLACE1007450  
 C-PLACE1007452  
 C-PLACE1007460  
 C-PLACE1007484  
 55 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734  
 C-PLACE1007507  
 C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728



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C-PLACE1007524  
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//  
1485bp//98%//AF159164  
C-PLACE1007544  
5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//  
P34537  
C-PLACE1007583  
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676  
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194  
10 C-PLACE1007621  
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506  
C-PLACE1007645  
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194  
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
15 8.7E-09//279aa//28%//Q26457  
C-PLACE1007690  
C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535  
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243  
C-PLACE1007725  
20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265  
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//  
AB014585  
C-PLACE1007746  
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602  
25 C-PLACE1007810  
C-PLACE1007843  
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//  
99%//AP000010  
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309  
30 C-PLACE1007897  
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//  
25%//Q99323  
C-PLACE1007954  
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//  
35 AF084530  
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//  
99%//AF079529  
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//  
48%//P52272  
40 C-PLACE1007990  
C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-  
SITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622  
C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
1833bp//99%//AC005628  
45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
CLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590  
C-PLACE1008095  
C-PLACE1008122  
C-PLACE1008129  
50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//  
31%//Q09531  
C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709  
C-PLACE1008209  
C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//  
55 671aa//77%//P53620  
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689  
C-PLACE1008280  
C-PLACE1008309

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C-PLACE1008329  
C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579  
C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432  
C-PLACE1008401  
5 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541  
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527  
C-PLACE1008457  
C-PLACE1008465  
10 C-PLACE1008488  
C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%//AL031778  
C-PLACE1008531  
15 C-PLACE1008532  
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620  
C-PLACE1008568  
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199  
20 C-PLACE1008621  
C-PLACE1008626  
C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
C-PLACE1008629  
25 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333  
C-PLACE1008693  
C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406  
30 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345  
C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974  
C-PLACE1008813  
35 C-PLACE1008854  
C-PLACE1008867  
C-PLACE1008887  
C-PLACE1008902  
C-PLACE1008925  
40 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623  
C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
C-PLACE1009045  
C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582  
C-PLACE1009090  
45 C-PLACE1009091  
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432  
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814  
C-PLACE1009110  
50 C-PLACE1009111  
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086  
C-PLACE1009158  
C-PLACE1009166  
55 C-PLACE1009174  
C-PLACE1009186  
C-PLACE1009190  
C-PLACE1009230

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C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295  
 C-PLACE1009328  
 C-PLACE1009335  
 5 C-PLACE1009338  
 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067  
 C-PLACE1009375  
 C-PLACE1009388  
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047//  
 10 165aa//33%//Q09820  
 C-PLACE1009434  
 C-PLACE1009443  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
 NASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356  
 15 C-PLACE1009459  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319  
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40//  
 179aa//37%//P34580  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FAC-  
 20 TOR).//8.1E-99//228aa//75%//Q99418  
 C-PLACE1009542  
 C-PLACE1009571  
 C-PLACE1009581  
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808  
 25 C-PLACE1009607  
 C-PLACE1009621  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%//  
 P55161  
 30 C-PLACE1009665  
 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN  
 CHROMOSOME I.//7E-33//166aa//43%//Q09876  
 C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200  
 35 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120  
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp//  
 100%//AB012190  
 C-PLACE1009794  
 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712  
 40 C-PLACE1009886  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-  
 108//277aa//43%//P53145  
 C-PLACE1009971  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%//  
 45 P28175  
 C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%//  
 AL080122  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//  
 736bp//73%//U48288  
 50 C-PLACE1010023  
 C-PLACE1010031  
 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482  
 C-PLACE1010076  
 55 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671  
 C-PLACE1010102  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//O04652  
 C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

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99%//AL049385  
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082  
 5 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662  
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130  
 C-PLACE1010202  
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722  
 10 C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%//AL080122  
 C-PLACE1010293  
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%//P52178  
 15 C-PLACE1010324  
 C-PLACE1010329  
 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.000000002//126aa//29%//P34024  
 C-PLACE1010364  
 20 C-PLACE1010383  
 C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643  
 C-PLACE1010491  
 C-PLACE1010492  
 25 C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%//AB022718  
 C-PLACE1010529  
 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//P253 86  
 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546  
 30 C-PLACE1010616  
 C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642  
 C-PLACE1010629  
 C-PLACE1010630  
 35 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755  
 C-PLACE1010714  
 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%//AB019987  
 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//AF020267  
 40 C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061  
 C-PLACE1010786  
 C-PLACE1010800  
 C-PLACE1010811  
 45 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%//Q05481  
 C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182  
 C-PLACE1010900  
 C-PLACE2000050  
 50 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-//2.4E-191//828aa//48%//P21783  
 C-PLACE4000590  
 C-PLACE4000638  
 55 C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aa//34%//P49816  
 C-Y79AA1001647

## Homology Search Result Data 7.

**[0315]** The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-  
PLE 16).

5 **[0316]** Data include

the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
10 the organism and the Accession No. of the top hit data, as in the order separated by //.

**[0317]** Data are not shown for the clones in which the P-value was higher than 1.

15 F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G).//0.13//52//38//P25860  
F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
64E).//2.2e-28//104//59//Q24574  
F-HEMBA1003854//VERPROLIN.//0.012//138//31//P37370  
F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT).//0.93//39//  
20 33//Q37131  
F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.90//20//50//P38524  
F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16).//7.6e-46//141//58//Q15973  
F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT).//0.0033//32//46//P70560  
F-HEMBA1006092//VERPROLIN.//1.0//62//35//P37370  
25 F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10).//0.30//41//36//P12350  
F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.089//21//52//Q02593  
F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).//0.38//156//30//P28697  
F-HEMBA100672  
F-HEMBA1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16012  
30 F-HEMBA1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//3.7e-54//  
241//47//P47853  
F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3).//0.59//48//39//Q51483  
F-MAMMA1002094  
F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58//27//P06333  
35 F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.9e-20//83//48//P10895  
F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326  
F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
PRECURSOR (ALS).//6.0e-23//207//32//O02833  
40 F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267  
F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P13816  
F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793  
F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722  
F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844  
45 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q01644  
F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q99014  
F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//4.0e-13//177//  
28//P16372  
F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.37//12//75//P53820  
50 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3).//0.99//61//32//Q42616  
F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666  
F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884  
F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//P37209  
F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303  
55 F-NT2RP2004095  
F-NT2RP2004732  
F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55//Q48251  
F-NT2RP2005454

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F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003  
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323  
 F-NT2RP2005882  
 5 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217  
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276  
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204  
 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).//0.064//110//34//P39881  
 10 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95//29//P15583  
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29//P17437  
 15 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162  
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124//31//P28284  
 F-OVARC1001029  
 20 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377  
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845  
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).//3.2e-08//205//24//P53046  
 25 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

## Homology Search Result Data 8.

30 **[0318]** The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.  
**[0319]** Data include

35 the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

40 **[0320]** Data are not shown for the clones in which the P-value was higher than 1.

40 F-HEMBA1000497  
 F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710  
 F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces.//1.7e-05//412//61//AC005081  
 45 F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386  
 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953  
 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641  
 50 F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851  
 F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738  
 F-HEMBA1006406//HS\_2268\_B2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566  
 55 F-HEMBA1006650//H.sapiens CpG island DNA genomic MseI fragment, clone 5h5, forward read cpg5h5.f1a.//9.4e-24//143//96//Z55730  
 F-HEMBA1006812//X.laevis xUBFalpal mRNA for upstream binding factor 2.//0.96//234//64//X59863

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F-HEM BB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158  
F-HEM BB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760  
5 F-HEM BB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127  
F-MAM MA1001252  
F-MAM MA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993  
10 F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136  
F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108  
F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199  
15 F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961  
F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411  
F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670  
20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827  
F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812  
F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622  
F-NT2RP2001214  
25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189  
F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589  
F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094  
30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097  
F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22//377//69//AP000018  
F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050  
35 F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476  
F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233  
F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698  
40 F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035  
F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970  
F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410  
45 F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770  
F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652  
F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242  
50 F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775  
F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cpg13g5.rt1a.//2.2e-18//163//85//Z56771  
55 F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.3e-76//351//86//AC005180  
F-NT2RP3003155  
F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

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F-OVARC1000008///0.0040//674//57//M82836  
 F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461  
 F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221  
 F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769  
 F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427  
 F-PLACE1003030  
 F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081  
 F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//3.1e-39//214//98//AL031660

## Homology Search Result Data 9.

**[0321]** The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

**[0322]** Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0323]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

**[0324]** Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567  
 R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785  
 R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281  
 R-HEMBA1004193//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567  
 R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241  
 R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598  
 R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//AC004678  
 R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282  
 R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574  
 R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071  
 R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.8e-55//430//81//Z82207  
 R-HEMBA100672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//AC006166  
 R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593  
 R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 unordered pieces.//0.00097//410//59//AC004688  
 R-MAMMA1001252//Homo sapiens clone 201104, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 unordered pieces.//2.9e-13//364//64//AC004529  
 R-MAMMA1002094//HS\_3163\_A1\_A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441



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R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1-6e-21//283//73//AC005258  
R-NT2RM4000657  
R-NT2RM4000783  
5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073  
R-NT2RM4001178  
R-NT2RM4002420  
10 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307  
R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043  
R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.0058//166//69//AC005324  
15 R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822  
R-NT2RP2001460  
R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228  
20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181  
R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168  
R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X \*.//5.3e-39//449//72//Z81014  
25 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0.0097//498//59//AC005412  
R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754  
30 R-NT2RP2003799//3.6e-05//408//60//AL010237  
R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//2.1e-10//455//61//AL034557  
R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287  
35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//315//61//AC005219  
R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindDIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63//Z86062  
40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//AC005232  
R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368  
R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348  
45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560  
R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466  
R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.8e-44//307//86//AC005180  
R-NT2RP3003155  
50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351  
R-OVARC1000008  
R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161  
55 R-OVARC1000751//HS\_2222\_A2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143  
R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

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R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

5 R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.1e-88//497//91//AL031660

10 Homology Search Result Data 10.

[0325] The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

[0326] Data include

15

the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

20

[0327] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

25

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element; mRNA sequence.//3.7e-06//140//70//AA749151

30

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

35

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element; mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR: 002710 002710 GAG POLYPROTEIN ; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

40

F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE: 415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA100672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR: 001940 001940 STRAWBERRY NOTCH ; mRNA sequence.//1.2e-16//117//92//AI580023

45

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

50

F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

55

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE: 2367501 3' similar to contains element L1 L1 repetitive element ; mRNA sequence.//1.4e-13//127//84//AI742251

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F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997  
 F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA se-  
 quence.//5.0e-07//116//71//AA017066  
 F-NT2RP2000660//qx01g11.x1 NCI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA se-  
 5 quence.//0.027//120//65//AI225283  
 F-NT2RP2001214  
 F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA se-  
 quence.//0.0013//89//78//AI651878  
 F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'  
 10 similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//2.3e-18//120//93//AA427992  
 F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains  
 Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687  
 F-NT2RP2002677  
 F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491  
 15 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//1.9e-19//229//76//AA705059  
 F-NT2RP2002843//wt88d12.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR:  
 P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//314//67//  
 AI964055  
 F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA se-  
 20 quence.//0.38//106//68//AI763133  
 F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//  
 91//AL049979  
 F-NT2RP2004095  
 F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691  
 25 F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR:  
 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ; mRNA sequence.//0.0020//220//61//AI969546  
 F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194  
 F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770  
 F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mR-  
 30 NA sequence.//2.0e-05//385//62//Z78328  
 F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362  
 F-NT2RP3001282  
 F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to con-  
 tains MSR1.t1 TAR1 TAR1 repetitive element ; mRNA sequence.//2.6e-07//245//66//AW008782  
 35 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA se-  
 quence.//0.58//164//64//R46086  
 F-NT2RP3003155  
 F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997  
 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565  
 40 F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541  
 F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802  
 F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to con-  
 tains element L1 repetitive element ; mRNA sequence.//0.0012//145//68//AI252422  
 F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA se-  
 45 quence.//7.1e-31//275//76//AA868469  
 F-PLACE1003030  
 F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//  
 1.2e-57//737//67//AJ010046  
 F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3',  
 50 mRNA sequence.//2.2e-21//216//76//H52716

Homology Search Result Data 11.

55 **[0328]** The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones  
 selected in EXAMPLE 16.).

**[0329]** Data include

the name of clone,

title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

- 5 **[0330]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.  
**[0331]** Data are not shown for the clones in which the P-value was higher than 1.
- 10 R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains  
Alu repetitive element;contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83//  
AA614254
- R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
278971 3', mRNA sequence.//0.004511193//63//N63303
- R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//  
80//AL049263
- 15 R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-  
tains Alu repetitive element;contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81//  
AI914747
- R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA  
sequence.//0.017//118//69//AI218308
- 20 R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-  
quence.//4.6e-111//522//99//AI861830
- R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5',  
mRNA sequence.//1.2e-22//295//72//AL041450
- 25 R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE: 1949489  
3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963
- R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-//76//AB018295
- R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630
- R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087
- 30 R-HEMBA100672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//  
74//AL096734
- R-HEMBA1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar  
to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788
- R-HEMBA1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321
- 35 R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-  
tains Alu repetitive element;contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91//  
AA504355
- R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mR-  
NA sequence.//2.5e-68//328//99//AI936520
- 40 R-NT2RM4000634//DKFZp434F2016\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3',  
mRNA sequence.//8.2e-20//185//81//AL041146
- R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992
- R-NT2RM4000783
- R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136
- 45 R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA se-  
quence.//0.77//96//62//AI457506
- R-NT2RM4002420//wl58b04.x1 NCI\_CGAP\_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA se-  
quence.//2.4e-85//438//94//AI857508
- R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA se-  
quence.//1.9e-45//270//91//AA738352
- 50 R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA se-  
quence.//3.3e-53//311//85//AI417680
- R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA se-  
quence.//4.3e-26//142//97//AA805691
- 55 R-NT2RP2001214//tw65g08.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains  
element MSR1 repetitive element ; mRNA sequence.//1.5e-57//289//97//AI680174
- R-NT2RP2001460
- R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'

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- similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//6.0e-13//85//96//AA427992  
R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA  
sequence.//0.0016//208//65//R22302
- 5 R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096  
R-NT2RP2002755//qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3',  
mRNA sequence.//1.5e-26//419//66//AI190698  
R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to  
contains L1.t1 L1 repetitive element; mRNA sequence.//1.8e-45//463//74//AI749673
- 10 R-NT2RP2003101//ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA se-  
quence.//7.5e-73//347//99//AI758824  
R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294  
R-NT2RP2004095//zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to con-  
tains element MER32 repetitive element ; mRNA sequence.//9.6e-07//188//66//AA436455
- 15 R-NT2RP2004732//tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to con-  
tains Alu repetitive element;contains element L1 repetitive element ; mRNA sequence.//4.3e-25//414//68//  
AI678956  
R-NT2RP2004920//wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA se-  
quence.//6.8e-91//483//93//AI694022
- 20 R-NT2RP2005454//yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
279616 3', mRNA sequence.//0.0070//325//59//N48302  
R-NT2RP2005776//qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1939307 3',  
mRNA sequence.//7.5e-08//89//82//AI338419  
R-NT2RP2005806//wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to con-  
tains MER2.b3 MER2 repetitive element ; mRNA sequence.//3.2e-16//235//71//AI671398
- 25 R-NT2RP2005882//wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA se-  
quence.//0.00095//352//59//AI925528  
R-NT2RP3001282//wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199  
R-NT2RP3001723//wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA se-  
quence.//4.2e-98//471//98//AI926617
- 30 R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mR-  
NA sequence.//9.2e-50//329//87//AL037910  
R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668  
3', mRNA sequence.//1.4e-30//159//99//AA173172
- 35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594  
R-OVARC1000008//wa69e12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA  
sequence.//1.0e-77//376//98//AI699393  
R-OVARC1000724//tf94b10.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA se-  
quence.//0.71//27//100//AI380236
- 40 R-OVARC1000751//og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA se-  
quence.//3.5e-13//274//63//AA863306  
R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar  
to contains Alu repetitive element;contains element PTR5 repetitive element ; mRNA sequence.//3.5e-13//175//74//  
N99464
- 45 R-PLACE1000814//tg49a08.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar  
to contains L1.t2 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//AI424789  
R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
cds.//4.0e-34//225//90//AF032387  
R-PLACE1005549//tm26b11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA  
sequence.//0.91//127//66//AI480253
- 50 R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5'  
similar to contains Alu repetitive element;contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87//  
R92256
- 55 Homology Search Result Data 12.

[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

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and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996

5 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344

C-HEMBA1000129//HYTOTHEICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884

C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738

10 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221

C-HEMBA1000231

C-HEMBA1000264

C-HEMBA1000280

C-HEMBA1000282

15 C-HEMBA1000303//&quot;Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.&quot;//7.1E-254//1440bp//87%//AF030131

C-HEMBA1000333//&quot;Homo sapiens mRNA for KIAA0874 protein, partial cds.&quot;//4.8E-253//1148bp//99%//AB020681

C-HEMBA1000351

20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//815bp//98%//AL050274

C-HEMBA1000396

C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357

C-HEMBA1000442

25 C-HEMBA1000456

C-HEMBA1000504

C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490

C-HEMBA1000519

C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755

30 C-HEMBA1000542//&quot;Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.&quot;//2.2E-194//663bp//83%//D89340

C-HEMBA1000545

C-HEMBA1000557

C-HEMBA1000592//&quot;Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.&quot;//0//1465bp//99%//AF121856

35 C-HEMBA1000594

C-HEMBA1000604

C-HEMBA1000622

C-HEMBA1000637

40 C-HEMBA1000655

C-HEMBA1000657//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.&quot;//7.2E-156//1366bp//76%//U35776

C-HEMBA1000749

C-HEMBA1000769

45 C-HEMBA1000773

C-HEMBA1000774

C-HEMBA1000822

C-HEMBA1000843

C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689

50 C-HEMBA1000870

C-HEMBA1000908

C-HEMBA1000934

C-HEMBA1000972

C-HEMBA1000986

55 C-HEMBA1000991

C-HEMBA1001008

C-HEMBA1001059//&quot;Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.&quot;//4.8E-169//786bp//99%//U06088

C-HEMBA1001094  
 C-HEMBA1001302//&quot;Homo sapiens calcium binding protein precursor, mRNA, complete cds.&quot;;/9.6E-258//682bp//94%//AF153686  
 C-HEMBA1001330  
 5 C-HEMBA1001497  
 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%//P19065  
 C-HEMBA1001570  
 10 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803  
 C-HEMBA1001640  
 C-HEMBA1001655  
 C-HEMBA1001672//&quot;Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.&quot;;/0//1707bp//98%//AF072247  
 15 C-HEMBA1001711  
 C-HEMBA1001723//&quot;Rattus norvegicus G beta-like protein GBL mRNA, complete cds.&quot;;/4.7E-172//1240bp//81%//AF051155  
 C-HEMBA1001746//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.&quot;;/7.6E-59//998bp//64%//AF098066  
 20 C-HEMBA1001781  
 C-HEMBA1001804//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.&quot;;/0//1637bp//99%//AF125158  
 C-HEMBA1001822//&quot;Mus musculus Ese2L protein mRNA, complete cds.&quot;;/1.9E-235//1329bp//89%//AF132479  
 25 C-HEMBA1001824  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332  
 C-HEMBA1001910  
 C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535  
 30 C-HEMBA1001921//&quot;Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.&quot;;/0//1850bp//99%//AF000145  
 C-HEMBA1001939  
 C-HEMBA1001950//&quot;Homo sapiens mRNA for KIAA0971 protein, complete cds.&quot;;/0//1974bp//99%//AB023188  
 35 C-HEMBA1001967//&quot;Homo sapiens NY-REN-57 antigen mRNA, partial cds.&quot;;/0//1721bp//99%//AF155114  
 C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089  
 C-HEMBA1002092//&quot;Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.&quot;;/1.3E-271//1583bp//88%//U92703  
 40 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357  
 C-HEMBA1002150  
 C-HEMBA1002151//&quot;Rattus norvegicus p34 mRNA, complete cds.&quot;;/1.1E-153//1059bp//82%//AF178669  
 45 C-HEMBA1002189  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226  
 C-HEMBA1002229  
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087  
 50 C-HEMBA1002341//&quot;Homo sapiens mRNA for KIAA0771 protein, partial cds.&quot;;/0//1514bp//99%//AB018314  
 C-HEMBA1002417//&quot;Homo sapiens chromosome 19, cosmid R28784, complete sequence.&quot;;/1.4E-299//294bp//100%//AC005954  
 C-HEMBA1002547//&quot;Homo sapiens agrin precursor mRNA, partial cds.&quot;;/0//1605bp//97%//AF016903  
 55 C-HEMBA1002703  
 C-HEMBA1002779  
 C-HEMBA1002816  
 C-HEMBA1002970

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C-HEMBA1002999//&quot;Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.  
&quot;//1.4E-171//1552bp//75%//U20286  
C-HEMBA1003021  
C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014  
5 C-HEMBA1003079  
C-HEMBA1003273  
C-HEMBA1003304  
C-HEMBA1003309  
C-HEMBA1003376  
10 C-HEMBA1003384  
C-HEMBA1003531  
C-HEMBA1003548  
C-HEMBA1003556  
C-HEMBA1003571  
15 C-HEMBA1003579  
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105  
C-HEMBA1003692  
C-HEMBA1003720  
C-HEMBA1003725  
20 C-HEMBA1003729  
C-HEMBA1003758  
C-HEMBA1003773//&quot;Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.  
&quot;//5.8E-81//511bp//86%//U17343  
C-HEMBA1003783//&quot;Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.&quot;//  
25 1.1E-190//1204bp//84%//AF084259  
C-HEMBA1003799  
C-HEMBA1003804  
C-HEMBA1003805//&quot;Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.&quot;//  
0//988bp//95%//AF090402  
30 C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484  
C-HEMBA1003856  
C-HEMBA1003866//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//1.2E-105//1192bp//70%//  
AF030430  
C-HEMBA1003879  
35 C-HEMBA1003880  
C-HEMBA1003893  
C-HEMBA1003908  
C-HEMBA1003937  
C-HEMBA1003942  
40 C-HEMBA1003958  
C-HEMBA1003976  
C-HEMBA1003978//&quot;Homo sapiens mRNA for KIAA0840 protein, partial cds.&quot;//0//1530bp//100%//  
AB020647  
C-HEMBA1003985  
45 C-HEMBA1004011  
C-HEMBA1004024  
C-HEMBA1004038  
C-HEMBA1004045  
C-HEMBA1004048  
50 C-HEMBA1004111//&quot;Homo sapiens mRNA for KIAA1276 protein, partial cds.&quot;//1.00E-163//751bp//  
99%//AB033102  
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141  
C-HEMBA1004138  
C-HEMBA1004143  
55 C-HEMBA1004150  
C-HEMBA1004168//&quot;Homo sapiens geminin mRNA, complete cds.&quot;//3.9E-208//951 bp//99%//  
AF067855  
C-HEMBA1004200



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C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%/P51153  
 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%/P40991  
 C-HEMBA1004238  
 5 C-HEMBA1004248//&quot;Homo sapiens insulin induced protein 2 mRNA, complete cds.&quot;//8.20E-175//  
 552bp//97%/AF125392  
 C-HEMBA1004272  
 C-HEMBA1004274  
 C-HEMBA1004275//&quot;Homo sapiens mRNA for KIAA1111 protein, partial cds.&quot;//0//1341bp//99%/AB029034  
 10 C-HEMBA1004286//&quot;Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.&quot;//  
 0//1982bp//99%/AF022795  
 C-HEMBA1004312  
 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%/Q99676  
 C-HEMBA1004323  
 15 C-HEMBA1004327  
 C-HEMBA1004330  
 C-HEMBA1004341  
 C-HEMBA1004366  
 C-HEMBA1004372  
 20 C-HEMBA1004389//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.  
 &quot;//0//1437bp//99%/AF125158  
 C-HEMBA1004394  
 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-  
 CLOPHILIN-10).//3.2E-32//148aa//52%/P52017  
 25 C-HEMBA1004429  
 C-HEMBA1004460  
 C-HEMBA1004461  
 C-HEMBA1004502  
 C-HEMBA1004554  
 30 C-HEMBA1004560  
 C-HEMBA1004610  
 C-HEMBA1004629  
 C-HEMBA1004632  
 C-HEMBA1004637  
 35 C-HEMBA1004670  
 C-HEMBA1004672  
 C-HEMBA1004697  
 C-HEMBA1004711  
 C-HEMBA1004725  
 40 C-HEMBA1004730  
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%/P42743  
 C-HEMBA1004751  
 C-HEMBA1004752  
 45 C-HEMBA1004889//&quot;Human C3f mRNA, complete cds.&quot;//6.70E-24//341aa//26%/U72515  
 C-HEMBA1004934  
 C-HEMBA1004944  
 C-HEMBA1004973  
 C-HEMBA1004977  
 50 C-HEMBA1005009//&quot;Homo sapiens BAF53a (BAF53a) mRNA, complete cds.&quot;//0//1813bp//99%/AF041474  
 C-HEMBA1005083  
 C-HEMBA1005113  
 C-HEMBA1005133  
 55 C-HEMBA1005185  
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%/P39929  
 C-HEMBA1005252//&quot;Homo sapiens mRNA for KIAA0585 protein, partial cds.&quot;//1.2E-268//1215bp//  
 99%/AB011157

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C-HEMBA1005296  
 C-HEMBA1005314  
 C-HEMBA1005331  
 C-HEMBA1005394  
 5 C-HEMBA1005403  
 C-HEMBA1005423//&quot;Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.  
 &quot;//2E-213//537bp//99%//AF041248  
 C-HEMBA1005468  
 C-HEMBA1005469  
 10 C-HEMBA1005474  
 C-HEMBA1005517  
 C-HEMBA1005518  
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809  
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929  
 15 C-HEMBA1005576//&quot;Homo sapiens mRNA for KIAA0463 protein, partial cds.&quot;//1.1E-181//835bp//  
 99%//AB007932  
 C-HEMBA1005582//&quot;TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL  
 TROPOMYOSIN).&quot;//0.00000009//213aa//27%//P09492  
 C-HEMBA1005583  
 20 C-HEMBA1005595//&quot;DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).&quot;//2.3E-54//562aa//29%//P34036  
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//  
 1448bp//99%//AL050012  
 C-HEMBA1005621//&quot;Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds.&quot;//2.9E-224//  
 1031bp//99%//AF139365  
 25 C-HEMBA1005666  
 C-HEMBA1005680  
 C-HEMBA1005685  
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//  
 4.4E-17//167aa//34%//P25296  
 30 C-HEMBA1005746  
 C-HEMBA1005755  
 C-HEMBA1005813  
 C-HEMBA1005822  
 C-HEMBA1005834  
 35 C-HEMBA1005884  
 C-HEMBA1005891  
 C-HEMBA1005909  
 C-HEMBA1005911  
 C-HEMBA1005931  
 40 C-HEMBA1005963  
 C-HEMBA1005991  
 C-HEMBA1006005  
 C-HEMBA1006031//&quot;Homo sapiens mRNA for putative phospholipase, complete cds.&quot;//0//1413bp//  
 99%//AB019435  
 45 C-HEMBA1006067  
 C-HEMBA1006081  
 C-HEMBA1006091  
 C-HEMBA1006100  
 C-HEMBA1006108//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//4.8E-245//764bp//  
 50 99%//AB023160  
 C-HEMBA1006121  
 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794  
 C-HEMBA1006155  
 C-HEMBA1006158//&quot;Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.&quot;//  
 55 //0//1551bp//99%//AF048693  
 C-HEMBA1006182  
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142  
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

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C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//  
 62aa//53%/P42698  
 C-HEMBA1006259  
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%/P10265  
 5 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
 FERASE).//1E-210//490aa//77%/P25500  
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//  
 30%/P32505  
 C-HEMBA1006284  
 10 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.2E-12//215aa//23%/P70473  
 C-HEMBA1006293  
 C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.4E-48//  
 248aa//43%/P38821  
 C-HEMBA1006349  
 15 C-HEMBA1006364  
 C-HEMBA1006381  
 C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."//2E-277//1729bp//  
 85%/U93563  
 C-HEMBA1006445//"Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds."//1.4E-  
 20 270//1224bp//100%/U96750  
 C-HEMBA1006483  
 C-HEMBA1006492  
 C-HEMBA1006497  
 C-HEMBA1006502  
 25 C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."//0//2334bp//99%/  
 AB014566  
 C-HEMBA1006535  
 C-HEMBA1006559//"Mus musculus PRAJA1 (Praja1) mRNA, complete cds."//2.8E-206//1107bp//83  
 %//U06944  
 30 C-HEMBA1006566  
 C-HEMBA1006579  
 C-HEMBA1006583  
 C-HEMBA1006612  
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.000000069//109aa//  
 35 38%/Q58323  
 C-HEMBA1006643  
 C-HEMBA1006674  
 C-HEMBA1006682  
 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
 40 INTERGENIC REGION.//3.3E-22//241aa//31%/P53196  
 C-HEMBA1006717  
 C-HEMBA1006744  
 C-HEMBA1006754  
 C-HEMBA1006767  
 45 C-HEMBA1006789  
 C-HEMBA1006832  
 C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."//0//  
 1467bp//96%/AB018566  
 C-HEMBA1006900  
 50 C-HEMBA1006926  
 C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%/  
 AJ010841  
 C-HEMBA1006973//"Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//  
 740bp//94%/AF004828  
 55 C-HEMBA1006993  
 C-HEMBA1007002  
 C-HEMBA1007062  
 C-HEMBA1007080

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C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626  
 C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//  
 99%//AL117450  
 C-HEMBA1007194//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.  
 5 &quot;//0//1588bp//99%//AF139658  
 C-HEMBA1007206  
 C-HEMBA1007256  
 C-HEMBA1007267  
 C-HEMBA1007281  
 10 C-HEMBA1007300//&quot;Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA,  
 splice variant 1, complete cds.&quot;//0//1519bp//99%//AF127479  
 C-HEMBA1007301  
 C-HEMBA1007319  
 C-HEMBA1007320  
 15 C-HEMBA1007327  
 C-HEMBA1007347  
 C-HEMBA1000005  
 C-HEMBA1000030  
 C-HEMBA1000048  
 20 C-HEMBA1000099  
 C-HEMBA1000141  
 C-HEMBA1000198  
 C-HEMBA1000217//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.  
 &quot;//0//1038bp//99%//AF090385  
 25 C-HEMBA1000218  
 C-HEMBA1000274  
 C-HEMBA1000312  
 C-HEMBA1000402  
 C-HEMBA1000420  
 30 C-HEMBA1000480  
 C-HEMBA1000530  
 C-HEMBA1000550  
 C-HEMBA1000556//&quot;Homo sapiens mRNA for KIAA0750 protein, complete cds.&quot;//6.3E-74//1213bp//  
 64%//AB018293  
 35 C-HEMBA1000586  
 C-HEMBA1000592  
 C-HEMBA1000593//&quot;Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.&quot;//1.3E-  
 107//503bp//99%//AF067864  
 C-HEMBA1000649  
 40 C-HEMBA1000693//&quot;Homo sapiens neuroan1 mRNA, complete cds.&quot;//0//2952bp//94%//AF040723  
 C-HEMBA1000822  
 C-HEMBA1000826  
 C-HEMBA1000890  
 C-HEMBA1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//  
 45 31%//P29122  
 C-HEMBA1001008  
 C-HEMBA1001020//&quot;Homo sapiens mRNA for KIAA0889 protein, complete cds.&quot;//0//1812bp//98%//  
 AB020696  
 C-HEMBA1001051  
 50 C-HEMBA1001112//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//6E-145//961bp//83%//  
 AF077032  
 C-HEMBA1001221  
 C-HEMBA1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938  
 C-HEMBA1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//  
 55 P16157  
 C-HEMBA1001302  
 C-HEMBA1001335  
 C-HEMBA1001337

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C-HEMBB1001356  
 C-HEMBB1001364  
 C-HEMBB1001366  
 C-HEMBB1001367  
 5 C-HEMBB1001527  
 C-HEMBB1001537  
 C-HEMBB1002359  
 C-HEMBB1002415  
 C-HEMBB1002457  
 10 C-HEMBB1002492  
 C-HEMBB1002495  
 C-HEMBB1002502  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%//P27544  
 C-HEMBB1002600//&quot;Homo sapiens tetraspan NET-5 mRNA, complete cds.&quot;//0//1417bp//99%//  
 15 AF089749  
 C-HEMBB1002607//&quot;Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.  
 &quot;//2E-136//660bp//98%//AF105421  
 C-HEMBB1002684  
 C-HEMBB1002692  
 20 C-HEMBB1002697  
 C-HEMBB1002705//&quot;Homo sapiens CGI-27 protein mRNA, complete cds.&quot;//7.80E-285//841bp//96%//  
 AF132961  
 C-MAMMA1000019  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%//  
 25 Z47553  
 C-MAMMA1000025  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226  
 C-MAMMA1000069  
 C-MAMMA1000084  
 30 C-MAMMA1000139  
 C-MAMMA1000163  
 C-MAMMA1000171  
 C-MAMMA1000173//&quot;Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete  
 cds.&quot;//2.6E-164//1044bp//87%//AF197060  
 35 C-MAMMA1000277  
 C-MAMMA1000278  
 C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%//X99836  
 C-MAMMA1000309  
 C-MAMMA1000312  
 40 C-MAMMA1000313  
 C-MAMMA1000361  
 C-MAMMA1000388//&quot;Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.&quot;//  
 0//1466bp//99%//AB015132  
 C-MAMMA1000395  
 45 C-MAMMA1000410  
 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//  
 53%//Q09232  
 C-MAMMA1000421  
 C-MAMMA1000422  
 50 C-MAMMA1000468  
 C-MAMMA1000472  
 C-MAMMA1000490  
 C-MAMMA1000524  
 C-MAMMA1000567  
 55 C-MAMMA1000612//&quot;Rattus norvegicus G beta-like protein GBL mRNA, complete cds.&quot;//1E-95//  
 1115bp//72%//AF051155  
 C-MAMMA1000623  
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

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C-MAMMA1000664  
 C-MAMMA1000670  
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//4.4E-33//250aa//  
 33%//P42660  
 5 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16)//7.70E-17//246aa//29%//P94524  
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1E-77//395aa//45%//  
 014646  
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779  
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//  
 10 55%//P87115  
 C-MAMMA1000746  
 C-MAMMA1000775  
 C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500  
 C-MAMMA1000831  
 15 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//7.8E-40//101aa//54%//027540  
 C-MAMMA1000842  
 C-MAMMA1000843  
 C-MAMMA1000856  
 C-MAMMA1000865  
 20 C-MAMMA1000875  
 C-MAMMA1000906  
 C-MAMMA1000908  
 C-MAMMA1000914  
 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711  
 25 C-MAMMA1000968  
 C-MAMMA1000979  
 C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//  
 1263bp//99%//AF117892  
 C-MAMMA1001021  
 30 C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN)  
 (FODRIN BETA CHAIN) (SPTBN1)."//1.6E-16//113aa//41%//Q01082  
 C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946  
 C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//  
 AF151830  
 35 C-MAMMA1001078  
 C-MAMMA1001091  
 C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P51521  
 C-MAMMA1001110  
 C-MAMMA1001126  
 40 C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273  
 C-MAMMA1001143  
 C-MAMMA1001154  
 C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338  
 C-MAMMA1001215  
 45 C-MAMMA1001244  
 C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//  
 89%//AF184275  
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.1E-52//630aa//  
 30%//P34537  
 50 C-MAMMA1001343  
 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//  
 99%//AL080121  
 C-MAMMA1001419  
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//  
 55 6.5E-129//260aa//92%//P52623  
 C-MAMMA1001510  
 C-MAMMA1001522  
 C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//

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M61764  
 C-MAMMA1001604  
 C-MAMMA1001620  
 C-MAMMA1001635  
 5 C-MAMMA1001649  
 C-MAMMA1001686  
 C-MAMMA1001692  
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR)//8.5E-32//171aa//36%//  
 P21573  
 10 C-MAMMA1001754//&quot;Homo sapiens CGI-11 protein mRNA, complete cds.&quot;//0//1837bp//98%//  
 AF132945  
 C-MAMMA1001757  
 C-MAMMA1001764  
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156//3.8E-45//351aa//38%//Q58556  
 15 C-MAMMA1001771//M.musculus mRNA for semaphorin B//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001790  
 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29)//2.6E-77//507aa//38%//Q07230  
 C-MAMMA1001858  
 C-MAMMA1001868//TRICHOHYALIN//2.7E-19//359aa//25%//P22793  
 20 C-MAMMA1001970  
 C-MAMMA1002042  
 C-MAMMA1002068  
 C-MAMMA1002153  
 C-MAMMA1002156  
 25 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)//6E-66//157aa//70%//P15880  
 C-MAMMA1002174  
 C-MAMMA1002209  
 C-MAMMA1002219//&quot;Homo sapiens mRNA for KIAA1067 protein, partial cds.&quot;//1.1E-181//861bp//  
 98%//AB028990  
 30 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-  
 CHANGE FACTOR)//8.8E-217//310aa//86%//P70541  
 C-MAMMA1002243  
 C-MAMMA1002268//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//1E-190//  
 1624bp//76%//AF068748  
 35 C-MAMMA1002269  
 C-MAMMA1002292  
 C-MAMMA1002294  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein//1.1E-214//881bp//97%//  
 AJ011679  
 40 C-MAMMA1002312  
 C-MAMMA1002329//M.musculus mRNA for semaphorin B//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002333  
 C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN//0.000078//127aa//26%//P40882  
 C-MAMMA1002353  
 45 C-MAMMA1002355  
 C-MAMMA1002356  
 C-MAMMA1002362  
 C-MAMMA1002380  
 C-MAMMA1002384  
 50 C-MAMMA1002427  
 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)//1E-11//128aa//36%//  
 P47623  
 C-MAMMA1002485//&quot;Homo sapiens stanniocalcin-related protein mRNA, complete cds.&quot;//0//1822bp//  
 99%//AF098462  
 55 C-MAMMA1002494  
 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION//1.2E-34//  
 337aa//31%//P43571  
 C-MAMMA1002530//&quot;Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

cds.&quot;0//1910bp//99%//AF065214  
 C-MAMMA1002554  
 C-MAMMA1002585//&quot;Homo sapiens mRNA for KIAA0860 protein, complete cds.&quot;0//1405bp//99%//  
 5 AB020667  
 C-MAMMA1002598  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//9.5E-16//159aa//37%//Q09931  
 C-MAMMA1002655//&quot;Homo sapiens mRNA for ganglioside sialidase, complete cds.&quot;0//1515bp//  
 10 99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.1E-45//618aa//26%//P27550  
 C-MAMMA1002673  
 C-MAMMA1002684//&quot;Homo sapiens mRNA for KIAA0214 protein, complete cds.&quot;0//3174bp//99%//  
 15 D86987  
 C-MAMMA1002711  
 C-MAMMA1002769//&quot;Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete  
 cds.&quot;2.2E-25//330bp//77%//AF011794  
 C-MAMMA1002775  
 20 C-MAMMA1002782  
 C-MAMMA1002796  
 C-MAMMA1002807  
 C-MAMMA1002838  
 C-MAMMA1002842//&quot;Mus musculus c-Cb1 associated protein CAP mRNA, complete cds.&quot;2.6E-58//  
 25 373bp//81%//U58883  
 C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.4E-160//  
 305aa//85%//P48059  
 C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.7E-30//214aa//  
 35 35%//P48060  
 C-MAMMA1002886  
 C-MAMMA1002890  
 C-MAMMA1002938//&quot;Homo sapiens mRNA for KIAA0698 protein, complete cds.&quot;8.4E-252//1139bp//  
 100%//AB014598  
 C-MAMMA1002964  
 40 C-MAMMA1003011//HESTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874  
 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//P06746  
 C-MAMMA1003015  
 C-MAMMA1003019  
 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-  
 45 DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//33%//P23851  
 C-MAMMA1003039  
 C-MAMMA1003044  
 C-MAMMA1003049  
 C-MAMMA1003056  
 50 C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%//Q60584  
 C-MAMMA1003066  
 C-MAMMA1003099  
 C-MAMMA1003104  
 C-MAMMA1003113//&quot;Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.&quot;1.1E-234//1178bp//86%//AF071316  
 55 C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%//P46735  
 C-MAMMA1003135  
 C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.3E-218//996bp//99%//Y15062  
 C-MAMMA1003150//&quot;Homo sapiens mRNA for KIAA1096 protein, partial cds.&quot;0//1342bp//99%//  
 AB029019  
 C-MAMMA1003166//&quot;Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.&quot;3.10E-158//592bp//97%//AF123052  
 C-NT2RM1000032



C-NT2RM1000035//&quot;Human mRNA for KIAA0199 gene, partial cds.&quot;//0//2948bp//99%//D83782  
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)  
 (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596  
 5 C-NT2RM1000055//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//3111bp//99%//  
 AB020636  
 C-NT2RM1000059  
 C-NT2RM1000062  
 C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 10 C-NT2RM1000119  
 C-NT2RM1000127  
 C-NT2RM1000131//&quot;Homo sapiens mRNA for KIAA0792 protein, complete cds.&quot;//0//2980bp//99%//  
 AB018335  
 C-NT2RM1000132//&quot;Homo sapiens NADH:ubiquinone oxidoreductas NDUF56 subunit mRNA, nuclear gene  
 15 encoding mitochondrial protein, complete cds.&quot;//7.8E-110//516bp//99%//AF044959  
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902  
 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 20 SPAC10F6.02C.//1.1E-10//94aa//47%//042643  
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//  
 AJ245820  
 C-NT2RM1000244//&quot;Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.&quot;//2E-126//592bp//  
 99%//U81002  
 25 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882  
 C-NT2RM1000256//&quot;Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete  
 cds.&quot;//0//3012bp//99%//AB016789  
 C-NT2RM1000260//&quot;Human mRNA for KIAA0130 gene, complete cds.&quot;//0//3139bp//98%//D50920  
 C-NT2RM1000271  
 30 C-NT2RM1000300  
 C-NT2RM1000314//&quot;Human mRNA for KIAA0159 gene, complete cds.&quot;//0//4349bp//99%//D63880  
 C-NT2RM1000354//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//7.4E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//&quot;Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.&quot;//0//  
 35 1599bp//99%//AF152462  
 C-NT2RM1000365  
 C-NT2RM1000377//&quot;Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.&quot;//  
 3.2E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 40 0.000000019//67aa//31%//P53915  
 C-NT2RM1000399  
 C-NT2RM1000430//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 1.4E-185//1486bp//81%//AF084928  
 C-NT2RM1000555//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
 45 AB020692  
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//  
 30%//Q08372  
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636  
 C-NT2RM1000661//&quot;Homo sapiens translation initiation factor 4e mRNA, complete cds.&quot;//4.3E-210//  
 50 960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989  
 C-NT2RM1000672  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440  
 C-NT2RM1000699  
 55 C-NT2RM1000741//&quot;Homo sapiens mRNA for KIAA0567 protein, partial cds.&quot;//1.1E-295//1338bp//  
 99%//AB011139  
 C-NT2RM1000742//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
 AF027208

C-NT2RM1000746//&quot;Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.&quot;//  
 6.70E-227//1043bp//99%//AF141310  
 C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202  
 C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808  
 5 C-NT2RM1000780  
 C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.1E-98//571bp//89%//Z97207  
 C-NT2RM1000802  
 C-NT2RM1000811//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
 AF027208  
 10 C-NT2RM1000826//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
 AB020692  
 C-NT2RM1000829  
 C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//  
 P16157  
 15 C-NT2RM1000852//&quot;Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.  
 &quot;//0//2206bp//99%//AF077033  
 C-NT2RM1000857//&quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;//0//3716bp//99%//  
 AB023179  
 C-NT2RM1000874//&quot;Homo sapiens death effector domain-containing testicular molecule mRNA, complete  
 20 cds.&quot;//1.4E-244//1113bp//99%//AF043733  
 C-NT2RM1000882//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;//4.30E-122//  
 1394bp//69%//AF126799  
 C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//  
 30%//P34537  
 25 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700  
 C-NT2RM1000898//&quot;ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).&quot;//8.9E-26//229aa//29%//  
 P02583  
 C-NT2RM1000905//&quot;Homo sapiens HSPC021 mRNA, complete cds.&quot;//0//1480bp//99%//AF077207  
 30 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%//  
 P46577  
 C-NT2RM1000927  
 C-NT2RM1000962  
 C-NT2RM1000978  
 35 C-NT2RM1001003//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//  
 2230bp//99%//AF030233  
 C-NT2RM1001043  
 C-NT2RM1001066  
 C-NT2RM1001072//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAM-  
 40 MA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).&quot;//8.3E-47//  
 259aa//35%//P08487  
 C-NT2RM1001085//&quot;Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.  
 &quot;//3.7E-32//460bp//64%//AF053768  
 C-NT2RM1001102//&quot;Human HEM45 mRNA, complete cds.&quot;//2.3E-27//482bp//63%//U88964  
 45 C-NT2RM1001105  
 C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//  
 99%//AL049943  
 C-NT2RM2000420  
 C-NT2RM2000566//&quot;Homo sapiens integrin alpha-7 mRNA, complete cds.&quot;//0//2519bp//96%//  
 50 AF032108  
 C-NT2RM2000609  
 C-NT2RM2000612//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA,  
 complete cds.&quot;//2.6E-106//1069bp//74%//U35776  
 C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160  
 55 C-NT2RM2001588  
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440  
 C-NT2RM2001613//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2601bp//99%//  
 AF084458

C-NT2RM2001632//KES 1 PROTEIN.//1.40E-31//342aa//34%//P35844  
 C-NT2RM2001648//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2421bp//99%//  
 AF084458  
 5 C-NT2RM2001652//&quot;Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.&quot;//0//  
 2608bp//99%//AF111162  
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P20107  
 C-NT2RM2001664//&quot;Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete  
 cds.&quot;//0//2471bp//99%//AF044195  
 10 C-NT2RM2001668//&quot;Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product  
 ending in intron 11, complete cds.&quot;//6.2E-16//464bp//62%//AF083391  
 C-NT2RM2001671//&quot;Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.  
 &quot;//0//1843bp//94%//U21155  
 C-NT2RM2001675  
 C-NT2RM2001681  
 15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//  
 30%//Q09674  
 C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF103804  
 C-NT2RM2001696  
 C-NT2RM2001698//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//6.2E-  
 20 253//1170bp//99%//AB028600  
 C-NT2RM2001700//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-  
 CAD) (FRAGMENT).&quot;//5.7E-130//536aa//49%//P50544  
 C-NT2RM2001716  
 C-NT2RM2001723  
 25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//7.2E-16//381aa//27%//Q09931  
 C-NT2RM2001743//&quot;Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.&quot;//  
 0//1498bp//99%//AF011792  
 30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609  
 C-NT2RM2001760//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2379bp//99%//  
 AF084458  
 C-NT2RM2001768  
 C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742  
 35 C-NT2RM2001782//&quot;Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.  
 &quot;//0//1470bp//99%//AF135422  
 C-NT2RM2001784  
 C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//  
 99%//AL050118  
 40 C-NT2RM2001813  
 C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657  
 C-NT2RM2001839//&quot;Homo sapiens calumein (Calu) mRNA, complete cds.&quot;//0//2415bp//97%//  
 AF013759  
 C-NT2RM2001840  
 45 C-NT2RM2001855  
 C-NT2RM2001867//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//967bp//99%//  
 AB023160  
 C-NT2RM2001879  
 C-NT2RM2001983//&quot;Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.&quot;//0//  
 50 1658bp//98%//AF089816  
 C-NT2RM2002145//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 8.5E-191//1524bp//81%//AF084928  
 C-NT2RM4000027  
 C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146  
 55 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003  
 C-NT2RM4000155//&quot;THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--  
 TRNA LIGASE) (THRRS).&quot;//1.2E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBRIL-7 gene.//3.6E-21//785bp//60%//X67336

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C-NT2RM4000167//&quot;Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.&quot;//0//1946bp//99%//AF071592

C-NT2RM4000199

C-NT2RM4000200

5 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%//Q16600

C-NT2RM4000233//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//3.4E-231//1395bp//86%//AF030430

C-NT2RM4000244

C-NT2RM4000251

10 C-NT2RM4000265

C-NT2RM4000324

C-NT2RM4000327

C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292

C-NT2RM4000425

15 C-NT2RM4000433//&quot;Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.&quot;//4.1E-271//2085bp//77%//AF062476

C-NT2RM4000514

C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//007230

C-NT2RM4000532

20 C-NT2RM4000534

C-NT2RM4000603

C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808

C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//2.7E-146//420aa//60%//P27550

25 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168

C-NT2RM4000689

C-NT2RM4000698

C-NT2RM4000700

C-NT2RM4000712//&quot;Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.&quot;//1E-136//1104bp//77%//AF022789

30 C-NT2RM4000717

C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154

C-NT2RM4000734//&quot;Homo sapiens mRNA for KIAA0760 protein, partial cds.&quot;//0//2273bp//99%//AB018303

35 C-NT2RM4000741//&quot;Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.&quot;//0//2184bp//99%//D88208

C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676

C-NT2RM4000764

C-NT2RM4000778

40 C-NT2RM4000787

C-NT2RM4000790

C-NT2RM4000795//&quot;Homo sapiens mRNA for KIAA0951 protein, complete cds.&quot;//0//1847bp//96%//AB023168

C-NT2RM4000796

45 C-NT2RM4000798//&quot;Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.&quot;//0//2603bp//99%//AF084521

C-NT2RM4000813

C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682

50 C-NT2RM4000833

C-NT2RM4000848

C-NT2RM4000852

C-NT2RM4000855

C-NT2RM4000887

55 C-NT2RM4000895

C-NT2RM4000950

C-NT2RM4000979

C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//

100%//AL050092  
 C-NT2RM4001032  
 C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%//Q06138  
 C-NT2RM4001054//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//3.1E-190//1315bp//81%//  
 5 AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//  
 165aa//33%//Q09820  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.9E-86//292aa//  
 48%//Q09417  
 10 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704  
 C-NT2RM4001151  
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q27969  
 C-NT2RM4001160  
 C-NT2RM4001187  
 15 C-NT2RM4001191//&quot;Homo sapiens clone 24963 mRNA sequence, complete cds.&quot;//0//1950bp//99%//  
 AF131737  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742  
 C-NT2RM4001203//&quot;Homo sapiens mRNA for KIAA0839 protein, partial cds.&quot;//0//3047bp//99%//  
 AB020646  
 20 C-NT2RM4001204//&quot;Homo sapiens mRNA for KIAA1089 protein, partial cds.&quot;//0//2349bp//99%//  
 AB029012  
 C-NT2RM4001217//&quot;Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds.&quot;//  
 7.3E-148//1409bp//72%//AF059611  
 C-NT2RM4001256//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//4.30E-55//  
 25 289bp//77%//AF129131  
 C-NT2RM4001258  
 C-NT2RM4001309  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676  
 30 C-NT2RM4001316//&quot;ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.3) (MCAD).&quot;//2.3E-31//334aa//30%//P08503  
 C-NT2RM4001320//&quot;Homo sapiens mRNA for Neuroblastoma, complete cds.&quot;//1.8E-39//728bp//64%//  
 D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626  
 35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.1E-  
 30//265aa//33%//P53742  
 C-NT2RM4001347//&quot;Homo sapiens NY-REN-25 antigen mRNA, partial cds.&quot;//0//2300bp//99%//  
 AF155103  
 C-NT2RM4001371//&quot;Homo sapiens IDN3 mRNA, partial cds.&quot;//0//2524bp//99%//AB019494  
 40 C-NT2RM4001382//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//2.2E-237//1079bp//  
 99%//AF098799  
 C-NT2RM4001384  
 C-NT2RM4001410  
 C-NT2RM4001411//&quot;Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA,  
 45 complete cds.&quot;//0//1962bp//87%//AF020526  
 C-NT2RM4001412//&quot;Homo sapiens nGAP mRNA, complete cds.&quot;//0//1918bp//99%//AF047711  
 C-NT2RM4001414  
 C-NT2RM4001437  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
 50 1.4E-118//444aa//46%//P73505  
 C-NT2RM4001454  
 C-NT2RM4001455  
 C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737  
 C-NT2RM4001489//&quot;Homo sapiens mRNA for KIAA0685 protein, complete cds.&quot;//0//1810bp//99%//  
 55 AB014585  
 C-NT2RM4001522  
 C-NT2RM4001557//&quot;Homo sapiens mRNA for KIAA1040 protein, partial cds.&quot;//0//1547bp//97%//  
 AB028963

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C-NT2RM4001565  
 C-NT2RM4001566//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;//0//1900bp//99%//  
 AB029037  
 C-NT2RM4001582//&quot;Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.&quot;//  
 5 1.5E-284//1082bp//90%//AF071317  
 C-NT2RM4001592//&quot;Homo sapiens mRNA for KIAA1122 protein, partial cds.&quot;//0//2170bp//99%//  
 AB032948  
 C-NT2RM4001594  
 C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750  
 10 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600  
 C-NT2RM4001629//&quot;MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG  
 3).&quot;//1.5E-93//278aa//38%//Q13368  
 C-NT2RM4001650  
 C-NT2RM4001662  
 15 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//  
 410aa//42%//P37339  
 C-NT2RM4001682  
 C-NT2RM4001710  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141  
 20 C-NT2RM4001715  
 C-NT2RM4001731//&quot;Homo sapiens mRNA for KIAA1004 protein, partial cds.&quot;//0//1922bp//100%//  
 AB023221  
 C-NT2RM4001746  
 C-NT2RM4001754  
 25 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//  
 58%//Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164  
 C-NT2RM4001810//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//2377bp//99%//  
 AB020670  
 30 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346  
 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//325aa//37%//P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%//  
 P51523  
 C-NT2RM4001836  
 35 C-NT2RM4001841//&quot;Homo sapiens mRNA for KIAA0920 protein, complete cds.&quot;//0//1861bp//98%//  
 AB023137  
 C-NT2RM4001842  
 C-NT2RM4001856  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779  
 40 C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711  
 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//  
 36%//Q15404  
 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486  
 C-NT2RM4001922//&quot;Homo-sapiens mRNA for KIAA0957 protein, complete cds.&quot;//0//2165bp//99%//  
 45 AB023174  
 C-NT2RM4001930//&quot;Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6)  
 mRNA, complete cds.&quot;//0//1930bp//99%//AF102851  
 C-NT2RM4001940//&quot;Homo sapiens timeless homolog mRNA, complete cds.&quot;//0//2087bp//99%//  
 AF098162  
 50 C-NT2RM4001953  
 C-NT2RM4001965  
 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330  
 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//  
 P51523  
 55 C-NT2RM4001984  
 C-NT2RM4001987//&quot;NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM  
 180) [CONTAINS: N-CAM 140].&quot;//3.2E-17//281aa//30%//P16170  
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

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INTERGENIC REGION.//6.9E-94//589aa//35%//P42935  
 C-NT2RM4002018  
 C-NT2RM4002034//&quot;Homo sapiens hiwi mRNA, partial cds.&quot;//1.9E-53//1585bp//60%//AF104260  
 C-NT2RM4002044  
 5 C-NT2RM4002054  
 C-NT2RM4002063//&quot;Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.&quot;//0//1865bp//99%//U82267  
 C-NT2RM4002066//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.&quot;//1.50E-211//1123bp//71%//AF117755  
 10 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%//Q04652  
 C-NT2RM4002128  
 C-NT2RM4002140  
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014  
 C-NT2RM4002161//&quot;Homo sapiens laforin (EPM2A) mRNA, complete cds.&quot;//0//2671bp//99%//AF084535  
 15 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%//P21590  
 C-NT2RM4002189//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//6.2E-33//688aa//27%//P08640  
 C-NT2RM4002205//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//3E-37//122aa//72%//Q07803  
 20 C-NT2RM4002213//&quot;Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.&quot;//0//2452bp//100%//AF157028  
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%//P40809  
 C-NT2RM4002251//&quot;ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI).&quot;//2.2E-36//320aa//38%//P27808  
 25 C-NT2RM4002256  
 C-NT2RM4002266  
 C-NT2RM4002281  
 30 C-NT2RM4002287  
 C-NT2RM4002294  
 C-NT2RM4002301  
 C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %//P48778  
 C-NT2RM4002339  
 35 C-NT2RM4002344  
 C-NT2RM4002373//&quot;Homo sapiens mRNA for KIAA0649 protein, complete cds.&quot;//0//2666bp//99%//AB014549  
 C-NT2RM4002374  
 C-NT2RM4002383  
 40 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.3E-29//275aa//30%//P27095  
 C-NT2RM4002438//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//1.1E-49//611bp//70%//AF129131  
 C-NT2RM4002446  
 45 C-NT2RM4002452  
 C-NT2RM4002457  
 C-NT2RM4002460//&quot;ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].&quot;//0.0000016//226aa//24%//P51515  
 C-NT2RM4002493  
 50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%//Q00808  
 C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137  
 C-NT2RM4002558//&quot;Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.&quot;//0//1797bp//99%//AF055899  
 C-NT2RM4002567  
 55 C-NT2RM4002593  
 C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815  
 C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%//032038

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C-NT2RP1000324  
 C-NT2RP1000363//&quot;Homo sapiens mRNA for KIAA0638 protein, partial cds.&quot;//0//1345bp//99%//  
 AB014538  
 C-NT2RP1000418  
 5 C-NT2RP1000513//&quot;Human NifU-like protein (hNifU) mRNA, partial cds.&quot;//6.50E-171//516bp//99%//  
 U47101  
 C-NT2RP1000721  
 C-NT2RP1000730  
 C-NT2RP1000767  
 10 C-NT2RP1000836  
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//  
 33%//Q09531  
 C-NT2RP1000943  
 C-NT2RP1001033//&quot;Homo sapiens delta-tubulin mRNA, complete cds.&quot;//2.10E-285//1290bp//100%//  
 15 AF201333  
 C-NT2RP1001073//&quot;Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.  
 &quot;//8.1E-107//504bp//99%//AF182291  
 C-NT2RP1001199  
 C-NT2RP1001248  
 20 C-NT2RP1001253//&quot;Homo sapiens oscillin (hLn) mRNA, complete cds.&quot;//0//2020bp//99%//AF029914  
 C-NT2RP1001286  
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001310//&quot;Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear  
 25 gene for mitochondrial product.&quot;//0//1732bp//99%//AF176006  
 C-NT2RP1001361//&quot;Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA,  
 complete cds.&quot;//6.5E-116//541bp//100%//AF070652  
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22//  
 284aa//25%//P40074  
 30 C-NT2RP1001432  
 C-NT2RP2000040//&quot;Homo sapiens mRNA for KIAA0747 protein, partial cds.&quot;//0//2648bp//99%//  
 AB013290  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%//  
 AJ242730  
 35 C-NT2RP2000098  
 C-NT2RP2000108  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD  
 SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//  
 40 7.1E-12//213aa//23%//P35251  
 C-NT2RP2000289  
 C-NT2RP2000327  
 C-NT2RP2000337  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910  
 45 C-NT2RP2000459  
 C-NT2RP2000498  
 C-NT2RP2000758  
 C-NT2RP2001137  
 C-NT2RP2001149  
 50 C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370  
 C-NT2RP2001173//&quot;Homo sapiens mRNA for KIAA0480 protein, complete cds.&quot;//0//1780bp//99%//  
 AB007949  
 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-10//88aa//38%//  
 P18722  
 55 C-NT2RP2001196  
 C-NT2RP2001226  
 C-NT2RP2001268//&quot;Homo sapiens mRNA for KIAA0810 protein, partial cds.&quot;//0//3301bp//98%//  
 AB018353



C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG)  
 (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%/P28663  
 C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%/P20107  
 C-NT2RP2001312  
 5 C-NT2RP2001327//&quot;TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12  
 PROTEIN).&quot;//5.5E-116//311aa//71%/Q13829  
 C-NT2RP2001328  
 C-NT2RP2001366  
 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%/Q02817  
 10 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//  
 581aa//54%/P93647  
 C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y18004  
 C-NT2RP2001420//&quot;Mus musculus nuclear protein NIP45 mRNA, complete cds.&quot;//9E-112//742bp//  
 82%/U76759  
 15 C-NT2RP2001450  
 C-NT2RP2001467  
 C-NT2RP2001506  
 C-NT2RP2001511//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//3.2E-  
 297//2206bp//75 %//AF093097  
 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%/Y14494  
 C-NT2RP2001536//&quot;Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete  
 cds.&quot;//0//2326bp//99%/AF035586  
 C-NT2RP2001560//NAV2 PROTEIN.//0.00000015//219aa//27%/Q60992  
 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.2E-29//294aa//  
 25 31%/Q09837  
 C-NT2RP2001581  
 C-NT2RP2001597//&quot;RYANODINE RECEPTOR, CARDIAC MUSCLE.&quot;//0.000000036//127aa//36%/P  
 30957  
 C-NT2RP2001628  
 30 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-  
 GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%/P42897  
 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-  
 PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANS-  
 FERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%/P14324  
 35 C-NT2RP2001813  
 C-NT2RP2001883//&quot;Homo sapiens CGI-01 protein mRNA, complete cds.&quot;//0//2306bp//99%/  
 AF132936  
 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%/P53946  
 C-NT2RP2001947  
 40 C-NT2RP2001985//&quot;Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein  
 E6TP1 alpha mRNA, complete cds.&quot;//2.00E-38//435bp//67%/AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%/Q  
 08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
 45 1.7E-47//247aa//52%/P35331  
 C-NT2RP2002058//&quot;Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.&quot;//0//  
 2510bp//99%/AF083217  
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7//1.5E-294//1334bp//99%/AF052183  
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%/P18490  
 50 C-NT2RP2002079//&quot;HISTONE H1, GONADAL.&quot;//4.4E-11//214aa//34%/P02256  
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%/AJ007509  
 C-NT2RP2002185//&quot;Homo sapiens ubiquilin mRNA, complete cds.&quot;//0//1789bp//99%/AF176069  
 C-NT2RP2002193//&quot;Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.  
 &quot;//0//2809bp//99%/AB021868  
 55 C-NT2RP2002231  
 C-NT2RP2002235  
 C-NT2RP2002252//&quot;Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.&quot;//0//3118bp//  
 91%/L38621

C-NT2RP2002292  
 C-NT2RP2002408  
 C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171aa//27%//P30620  
 5 C-NT2RP2002498  
 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386  
 C-NT2RP2002520//&quot;Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.&quot;//3.70E-34//668bp//61%//AF105427  
 C-NT2RP2002549  
 10 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
 C-NT2RP2002706  
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194  
 C-NT2RP2002800  
 15 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922  
 C-NT2RP2002891  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%//Q18964  
 C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737  
 20 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
 C-NT2RP2003034  
 C-NT2RP2003099  
 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117  
 25 C-NT2RP2003157//&quot;Homo sapiens CGI-74 protein mRNA, complete cds.&quot;//0//2037bp//99%//AF151832  
 C-NT2RP2003158//&quot;Homo sapiens mRNA for proteasome subunit p58, complete cds.&quot;//0//2091bp//99%//D67025  
 C-NT2RP2003165  
 30 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
 C-NT2RP2003277//&quot;Homo sapiens mRNA for KIAA0625 protein, partial cds.&quot;//0//3788bp//99%//AB014525  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400  
 35 C-NT2RP2003297  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886  
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754  
 40 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769  
 C-NT2RP2003393  
 C-NT2RP2003445  
 C-NT2RP2003466//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;7//0//2194bp//99%//AF126799  
 45 C-NT2RP2003480//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.&quot;//0//3012bp//99%//AF125158  
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%//P04175  
 50 C-NT2RP2003511  
 C-NT2RP2003513//&quot;Human mRNA for KIAA0270 gene, partial cds.&quot;//0//2137bp//97%//D87460  
 C-NT2RP2003567//&quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&quot;//0//2343bp//99%//AB007931  
 55 C-NT2RP2003604//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//2442bp//99%//AF030233  
 C-NT2RP2003691  
 C-NT2RP2003713//&quot;Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.&quot;//0//2018bp//99%//AF073344

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C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//  
 80%//P53620  
 C-NT2RP2003764  
 C-NT2RP2003769  
 5 C-NT2RP2003777  
 C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%//  
 Q11076  
 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//  
 0.00000016//117aa//29%//Q91955  
 10 C-NT2RP2003981//&quot;Homo sapiens mRNA for KIAA0804 protein, partial cds.&quot;//0//3046bp//99%//  
 AB018347  
 C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//  
 99%//AL050367  
 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599  
 15 C-NT2RP2004066//&quot;Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete  
 sequence.&quot;//0//2410bp//99%//AL034555  
 C-NT2RP2004081  
 C-NT2RP2004124  
 C-NT2RP2004152  
 20 C-NT2RP2004165  
 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-  
 31//424aa//28%//007231  
 C-NT2RP2004239//&quot;Homo sapiens lok mRNA for protein kinase, complete cds.&quot;//0//3044bp//99%//  
 AB015718  
 25 C-NT2RP2004245  
 C-NT2RP2004364  
 C-NT2RP2004365  
 C-NT2RP2004366//&quot;Homo sapiens mRNA for KIAA0986 protein, partial cds.&quot;//0//2790bp//97%//  
 AB023203  
 30 C-NT2RP2004373  
 C-NT2RP2004476//&quot;Homo sapiens cyclin L ania-6a mRNA, complete cds.&quot;//0//2075bp//99%//  
 AF180920  
 C-NT2RP2004551  
 C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903  
 35 C-NT2RP2004600  
 C-NT2RP2004664//&quot;Homo sapiens mRNA for KIAA0460 protein, partial cds.&quot;//0//2368bp//99%//  
 AB007929  
 C-NT2RP2004743  
 C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//  
 40 190aa//41-%//P38692  
 C-NT2RP2004816//&quot;Homo sapiens H beta 58 homolog mRNA, complete cds.&quot;//0//2144bp//96%//  
 AF054179  
 C-NT2RP2004861  
 C-NT2RP2004897  
 45 C-NT2RP2004933//&quot;Homo sapiens mRNA for ZIP-kinase, complete cds.&quot;//0//2103bp//99%//AB007144  
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386  
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)  
 (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%//  
 Q92089  
 50 C-NT2RP2005162//&quot;Homo sapiens aspartyl aminopeptidase mRNA, complete cds.&quot;//0//1615bp//99%//  
 AF005050  
 C-NT2RP2005204//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.  
 &quot;//0//1262bp//99%//AF090385  
 C-NT2RP2005227  
 55 C-NT2RP2005287  
 C-NT2RP2005288//&quot;Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.&quot;//0//  
 2992bp//99%//AF060219  
 C-NT2RP2005490//&quot;Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.&quot;//1.8E-175//1102bp//

83%//AF053628  
 C-NT2RP2005539//&quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&quot;//0//1560bp//99%//AB020657  
 5 C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053  
 C-NT2RP2005722//&quot;Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.&quot;//0//2545bp//99%//AB011414  
 C-NT2RP2005732  
 10 C-NT2RP2005784//&quot;Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.&quot;//0//2191bp//92%//AF155120  
 C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004  
 C-NT2RP2005859//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//1649bp//99%//AB020670  
 15 C-NT2RP2006023  
 C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155  
 C-NT2RP2006441  
 C-NT2RP3000002  
 20 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481  
 C-NT2RP3000055  
 C-NT2RP3000068  
 C-NT2RP3000080  
 25 C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//P46401  
 C-NT2RP3000092  
 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692  
 30 C-NT2RP3000134  
 C-NT2RP3000149  
 C-NT2RP3000197  
 C-NT2RP3000207//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//2.9E-11//721aa//23%//P08640  
 35 C-NT2RP3000233//&quot;Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence.&quot;//0//1462bp//99%//AL035424  
 C-NT2RP3000235  
 C-NT2RP3000247  
 40 C-NT2RP3000267  
 C-NT2RP3000299//&quot;Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.&quot;//0//2730bp//82%//D29766  
 C-NT2RP3000324  
 C-NT2RP3000341//&quot;Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.&quot;//1.5E-246//1124bp//99%//AF106622  
 45 C-NT2RP3000393//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//5.8E-266//1373bp//86%//AF061817  
 C-NT2RP3000441//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.&quot;//3.40E-42//645bp//67%//AF098066  
 50 C-NT2RP3000449  
 C-NT2RP3000451  
 C-NT2RP3000456  
 C-NT2RP3000542  
 C-NT2RP3000561  
 55 C-NT2RP3000562//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//0//2165bp//99%//AF093097  
 C-NT2RP3000578//HES1 PROTEIN.//1-3E-22//229aa//27%//P35843  
 C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

C-NT2RP3000592  
 C-NT2RP3000622  
 C-NT2RP3000624  
 C-NT2RP3000685  
 5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//014153  
 C-NT2RP3000742//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA  
 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).&quot;//4.1E-165//  
 371aa//49%//P10895  
 C-NT2RP3000753  
 10 C-NT2RP3000826  
 C-NT2RP3000865  
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426  
 C-NT2RP3001007  
 C-NT2RP3001055  
 15 C-NT2RP300111//&quot;Homo sapiens TRF-proximal protein mRNA, complete cds.&quot;//1.50E-149//731bp//  
 97%//AF097725  
 C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737  
 C-NT2RP3001126  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154  
 20 C-NT2RP3001232  
 C-NT2RP3001268//&quot;Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.&quot;//0//  
 3606bp//99%//AF198358  
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//  
 1.3E-99//669bp//83%//Y18101  
 25 C-NT2RP3001274//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;//0//2254bp//99%//  
 AB028960  
 C-NT2RP3001281  
 C-NT2RP3001297  
 C-NT2RP3001318  
 30 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508  
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089  
 C-NT2RP3001374  
 C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270  
 35 C-NT2RP3001432  
 C-NT2RP3001447  
 C-NT2RP3001449//&quot;Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the  
 alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A,  
 -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA,  
 40 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal  
 Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)  
 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G  
 protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 complete sequence.&quot;//0//1827bp//99%//AL031282  
 45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-  
 ER 2).//3.2E-90//157aa//59%//P36371  
 C-NT2RP3001459  
 C-NT2RP3001527//&quot;Human Spl40 protein (Spl40) mRNA, complete cds.&quot;//4.3E-290//793bp//93%//  
 U63420  
 50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II.//9.10E-10//158aa//  
 31%//Q10022  
 C-NT2RP3001580//&quot;Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.&quot;/  
 //0//1730bp//85%//AF163665  
 C-NT2RP3001587//&quot;Human anthracycline-associated resistance ARX mRNA, complete cds.&quot;//0//  
 55 2617bp//99%//U35832  
 C-NT2RP3001589  
 C-NT2RP3001607  
 C-NT2RP3001608

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C-NT2RP3001671//&quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&quot;//0//2310bp//99%//AB020657

C-NT2RP3001672//&quot;Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.&quot;//0//2836bp//99%//AF149046

5 C-NT2RP3001678

C-NT2RP3001688//&quot;Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA, complete cds.&quot;//0//1695bp//99%//AF099013

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386

10 C-NT2RP3001698

C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%//P54356

C-NT2RP3001716

C-NT2RP3001752

15 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//55%//P52272

C-NT2RP3001844

C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//99%//AL050011

20 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.1E-125//302aa//60%//P55347

C-NT2RP3001898//&quot;Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.&quot;//0//1587bp//100%//AB000624

C-NT2RP3001931

25 C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709

C-NT2RP3002002

C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-19211475bp//94%//X86779

C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955

C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232

30 C-NT2RP3002045//&quot;Homo sapiens mRNA for KIAA0899 protein, partial cds.&quot;//0//33 85bp//99%//AB020706

C-NT2RP3002056//&quot;Homo sapiens Rb binding protein homolog mRNA, partial cds.&quot;//0//2374bp//99%//AF083249

35 C-NT2RP3002062//&quot;Homo sapiens mRNA for KIAA0873 protein, partial cds.&quot;//0//3764bp//99%//AB020680

C-NT2RP3002081//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.&quot;//4.1E-233//1896bp//69%//AF111423

C-NT2RP3002097

40 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387

C-NT2RP3002142

C-NT2RP3002146

C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.8E-253//474aa//93%//P15170

45 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7//1.9E-151//223aa//91%//Q02614

C-NT2RP3002166

C-NT2RP3002181

C-NT2RP3002244

C-NT2RP3002248

50 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978

C-NT2RP3002276

C-NT2RP3002304

C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792

55 C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%//AJ133421

C-NT2RP3002566

C-NT2RP3002587

C-NT2RP3002590

C-NT2RP3002631

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C-NT2RP3002650//&quot;Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.&quot;//0//2109bp//87%//AF165163  
C-NT2RP3002663//&quot;Homo sapiens putative glycolipid transfer protein mRNA, complete cds.&quot;//8.10E-263//1243bp//97%//AF103731  
5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2)//2.50E-73//179aa//36%//P13060  
C-NT2RP3002763  
C-NT2RP3002861  
C-NT2RP3002911  
C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN)//2E-111//551aa//42%//Q04652  
10 C-NT2RP3002953//&quot;Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.&quot;//0//2388bp//99%//AF152498  
C-NT2RP3002988//&quot;Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.&quot;//1.8E-292//1325bp//99%//AF080158  
C-NT2RP3003008  
15 C-NT2RP3003101//&quot;Mouse mRNA for tetracycline transporter-like protein, complete cds.&quot;//3.6E-83//807bp//72%//D88315  
C-NT2RP3003204  
C-NT2RP3003278  
C-NT2RP3003282//&quot;Homo sapiens dynamin (DNM) mRNA, complete cds.&quot;//0//2596bp//98%//L36983  
20 C-NT2RP3003290//&quot;Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.&quot;//1.5e-310//1468bp//82%//AB033922  
C-NT2RP3003302  
C-NT2RP3003313//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.&quot;//0//2476bp//99%//AF117657  
25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052)//1.3E-35//178aa//44%//Q62191  
C-NT2RP3003344  
C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION//2.80E-07//161aa//28%//P40084  
30 C-NT2RP3003377  
C-NT2RP3003385//&quot;Mus musculus SKD3 mRNA, complete cds.&quot;//0//2133bp//85%//U09874  
C-NT2RP3003433  
C-NT2RP3003490//&quot;Homo sapiens mRNA for KIAA0725 protein, partial cds.&quot;//0//2437bp//99%//AB018268  
35 C-NT2RP3003491//&quot;Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.&quot;//5.6E-36//842bp//62%//AF091624  
C-NT2RP3004206//CROOKED NECK PROTEIN//1.4E-220//567aa//67%//P17886  
C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene)//0//2445bp//100%//AJ245820  
40 C-NT2RP3004209//&quot;Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.&quot;//0//2320bp//99%//AF126736  
C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG)//4.7E-13//118aa//33%//P52734  
C-NT2RP3004246  
45 C-NT2RP3004258//&quot;Homo sapiens ZIS1 mRNA, complete cds.&quot;//0//1861bp//99%//AF065391  
C-NT2RP3004262//&quot;Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.&quot;//2.4E-248//1126bp//100%//AF088982  
C-NT2RP3004341  
C-NT2RP3004378  
50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene)//1E-66//364bp//93%//AJ007798  
C-NT2RP3004428  
C-NT2RP3004451  
C-NT2RP3004454//&quot;Homo sapiens mRNA for KIAA0448 protein, complete cds.&quot;//0//2875bp//99%//AB007917  
55 C-NT2RP3004472//GERM CELL-LESS PROTEIN//1.6E-61//170aa//40%//Q01820  
C-NT2RP3004498//&quot;Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.&quot;//2E-249//1777bp//80%//U83176  
C-NT2RP3004504//M.musculus mRNA for CPEB protein//1.9E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%/P40484  
 C-NT2RP3004534//&quot;Mouse oncogene (ect2) mRNA, complete cds.&quot;//0//2075bp//87%/L11316  
 C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%/P33755  
 5 C-NT2RP4000907//&quot;Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.&quot;//0//  
 2127bp//86%/D45913  
 C-NT2RP4001029//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//0//1711bp//  
 90%/U20086  
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//  
 186aa//29%/024076  
 10 C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%/P35844  
 C-NT2RP4001442  
 C-NT2RP4001529//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//1.70E-255//  
 1148bp//90%/U20086  
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%/P12868  
 15 C-OVARC1000106//&quot;TROPOMYOSIN 1, FUSION PROTEIN 33.&quot;//0.000032//165aa//27%/P49455  
 C-OVARC1000198  
 C-OVARC1000682//&quot;PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSI-  
 DASE 1B).&quot;//1.1E-209//293aa//95%/P39098  
 20 C-OVARC1000703  
 C-OVARC1000722//&quot;Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, com-  
 plete cds.&quot;//0//759bp//98%/AF038661  
 C-OVARC1000730  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%/P25159  
 25 C-OVARC1000781  
 C-OVARC1000787  
 C-OVARC10008347//Homo sapiens mRNA for atopy related autoantigen CALCJ/2.8E-258//1183bp//99%/Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%/P08199  
 C-OVARC1000850//&quot;Homo sapiens PB39 mRNA, complete cds.&quot;//0//2095bp//99%/AF045584  
 30 C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%/Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%/P40484  
 C-OVA-RC1000883  
 C-OVARC1000886  
 C-OVARC1000912  
 35 C-OVARC1000915//&quot;Homo sapiens histone deacetylase 5 mRNA, complete cds.&quot;//1.60E-121//591bp//  
 97%/AF132608  
 C-OVARC1000924  
 C-OVARC1000964  
 C-OVARC1000984  
 40 C-OVARC1001004  
 C-OVARC1001010  
 C-OVARC1001011  
 C-OVARC1001032  
 C-OVARC1001044  
 45 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%/P43490  
 C-OVARC1001068//&quot;Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.&quot;//0//1819bp//  
 99%/AF082657  
 C-OVARC1001074  
 C-OVARC1001092//&quot;Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 50 LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).&quot;//2E-214//769bp//97%/AJ005897  
 C-OVARC1001107//&quot;Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.&quot;//6.1E-  
 276//594bp//98%/AF167572  
 C-OVARC1001154//&quot;Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.&quot;//2.3E-296//  
 55 1561bp//93%/AF055008  
 C-OVARC1001161  
 C-OVARC1001167  
 C-OVARC1001170



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C-OVARC1001171//&quot;Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.&quot; //5.7E-151//436bp//92%//U94855  
C-OVARC1001173  
C-OVARC1001176  
5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510  
C-OVARC1001188  
C-OVARC1001232//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).&quot; //5.10E-22//83aa//37%//Q10568  
C-OVARC1001270  
10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).// 0.0000014//224aa//26%//P25976  
C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444  
C-OVARC1001344  
C-OVARC1001369  
15 C-OVARC1001372//&quot;Homo sapiens mRNA for KIAA0897 protein, partial cds.&quot; //0//840bp//97%// AB020704  
C-OVARC1001391  
C-OVARC1001399  
C-OVARC1001417//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.&quot; //0//1715bp//99%//AF135802  
20 C-OVARC1001419//&quot;Homo sapiens GOK (STIM1) mRNA, complete cds.&quot; //4.9E-48//586bp//69%// U52426  
C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111  
C-OVARC1001453  
25 C-OVARC1001476//&quot;Mus musculus YGR163w mRNA homologue, complete cds.&quot; //1.80E-187// 510bp//89%//AB017616  
C-OVARC1001480  
C-OVARC1001489  
C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161  
30 C-OVARC1001525  
C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081  
C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%// AF031165  
35 C-OVARC1001600  
C-OVARC1001610//&quot;Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.&quot; //0//1870bp//99%//AF068302  
C-OVARC1001702  
C-OVARC1001703//&quot;Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.&quot; //3.5E- 16//399bp//61%//AF133670  
40 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa// 38%//Q62267  
C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI- AZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106  
45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796  
C-OVARC1001731//&quot;TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.&quot; //4E-122// 282aa//85%//P08942  
C-OVARC1001745  
C-OVARC1001762//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).&quot; //6.4E-85//514aa//34%//P12945  
50 C-OVARC1001766//&quot;Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.&quot; //0//963bp//99%//U97670  
C-OVARC1001767//&quot;Homo sapiens mRNA for KIAA0675 protein, complete cds.&quot; //0//2083bp//99%// AB014575  
55 C-OVARC1001768  
C-OVARC1001791  
C-OVARC1001795  
C-OVARC1001802

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C-OVARC1001809//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//2.7E-190//  
 1624bp//76%//AF068748  
 C-OVARC1001828  
 C-OVARC1001846  
 5 C-OVARC1001861  
 C-OVARC1001879  
 C-OVARC1001880  
 C-OVARC1001883  
 C-OVARC1001916  
 10 C-OVARC1001928  
 C-OVARC1001942//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
 AMINO, ACETYLTRANSFERASE 1).&quot;//3.1E-81//497aa//35%//P12945  
 C-OVARC1001943//&quot;Mus musculus DEBT-91 mRNA, complete cds.&quot;//0//2035bp//87%//AF143859  
 C-OVARC1001950  
 15 C-OVARC1001987//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//  
 2.3E-220//652bp//84%//AF061817  
 C-OVARC1002050//&quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&quot;//0//  
 1019bp//99%//AB029290  
 C-OVARC1002082  
 20 C-OVARC1002107  
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//  
 035913  
 C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955  
 25 C-OVARC1002156  
 C-OVARC1002158  
 C-PLACE1000004//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//0//2365bp//99%//AB019602  
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643  
 C-PLACE1000048  
 30 C-PLACE1000050  
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154  
 C-PLACE1000081//&quot;Human SEC7 homolog Tic (TIC) mRNA, complete cds.&quot;//0//2077bp//99%//  
 U63127  
 C-PLACE1000094  
 35 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.8E-62//158aa//81%//P20290  
 C-PLACE1000214  
 C-PLACE1000236  
 C-PLACE1000246  
 40 C-PLACE1000292  
 C-PLACE1000308  
 C-PLACE1000332  
 C-PLACE1000453  
 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//  
 45 P51522  
 C-PLACE1000599  
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918  
 C-PLACE1000653//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//  
 0//1992bp//99%//AF180371  
 50 C-PLACE1000656//&quot;Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
 LLNLc110F1857Q7 (RZPD Berlin)).&quot;//2.1E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//&quot;Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.&quot;//  
 0//1366bp//99%//AF119043  
 C-PLACE1000712  
 55 C-PLACE1000749  
 C-PLACE1000769//&quot;Homo sapiens CGI-18 protein mRNA, complete cds.&quot;//0//1985bp//98%//  
 AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

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CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734  
 C-PLACE1000849  
 C-PLACE1000856//&quot;Homo sapiens mRNA for KIAA0974 protein, partial cds.&quot;//0//1310bp//100%//  
 5 AB023191  
 C-PLACE1000931  
 C-PLACE1000987//&quot;Homo sapiens mRNA for KIAA0724 protein, complete cds.&quot;//0//1749bp//99%//  
 AB018267  
 C-PLACE1001010  
 C-PLACE1001015  
 10 C-PLACE1001024  
 C-PLACE1001062//&quot;Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence.&quot;//  
 2.7E-32//470bp//71%//AC006020  
 C-PLACE1001104  
 C-PLACE1001168  
 15 C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496  
 C-PLACE1001185//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//1668bp//99%//  
 AB023160  
 C-PLACE1001238//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//  
 2E-202//1333bp//80%//D14336  
 20 C-PLACE1001280  
 C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X71642  
 C-PLACE1001304//&quot;Homo sapiens zinc finger protein dp mRNA, complete cds.&quot;//0//2421bp//99%//  
 AF153201  
 C-PLACE1001311  
 25 C-PLACE1001323  
 C-PLACE1001351  
 C-PLACE1001414  
 C-PLACE1001440  
 C-PLACE1001456  
 30 C-PLACE1001517//&quot;Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1),  
 complete cds.&quot;//4.60E-112//392bp//87%//AB002137  
 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809  
 C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//  
 P51523  
 35 C-PLACE1001634  
 C-PLACE1001640  
 C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408  
 C-PLACE1001705  
 C-PLACE1001716  
 40 C-PLACE1001720  
 C-PLACE1001745  
 C-PLACE1001748//&quot;Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.&quot;//0//2602bp//99%//  
 AF061243  
 C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein  
 45 TRP6.//0//2900bp//99%//AJ006276  
 C-PLACE1001799  
 C-PLACE1001845//&quot;Mus musculus cyclin ania-6a mRNA, complete cds.&quot;//3.30E-31//925bp//62%//  
 AF159159  
 C-PLACE1001897  
 50 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//  
 076094  
 C-PLACE1002157  
 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT  
 SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591  
 55 C-PLACE1002227  
 C-PLACE1002259  
 C-PLACE1002319  
 C-PLACE1002395//&quot;Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.&quot;//7.9E-

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100//966bp//75%//AB030505  
 C-PLACE1002477  
 C-PLACE1002493//&quot;Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.  
 &quot;//1.7E-113//545bp//98%//AF042273  
 5 C-PLACE1002500  
 C-PLACE1002514  
 C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396  
 C-PLACE1002537  
 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890  
 10 C-PLACE10025 83//&quot;GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE  
 RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).&quot;//5.6E-34//  
 76aa//98%//P39087  
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340  
 C-PLACE1002625  
 15 C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046  
 C-PLACE1002768  
 C-PLACE1002782//&quot;Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.&quot;//3.8E-43//  
 385bp//77%//U50927  
 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973  
 20 C-PLACE1002853  
 C-PLACE1002908//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//0//  
 1654bp//99%//AB028600  
 C-PLACE1002962  
 C-PLACE1002968  
 25 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091  
 C-PLACE1003025  
 C-PLACE1003027//&quot;Homo sapiens mRNA for KIAA0516 protein, partial cds.&quot;//2.1e-314//1417bp//  
 100%//AB011088  
 C-PLACE1003044//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//1382bp//96%//  
 30 AB020636  
 C-PLACE1003176  
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%//  
 Q15391  
 C-PLACE1003256  
 35 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa//47%//P21541  
 C-PLACE1003343  
 C-PLACE1003361  
 C-PLACE1003366//&quot;Homo sapiens otoferlin (OTOF) mRNA, complete cds.&quot;//1.4E-78//542bp//67%//  
 AF107403  
 40 C-PLACE1003373  
 C-PLACE1003375  
 C-PLACE1003394//&quot;Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.&quot;//2.30E-150//  
 774bp//94%//M83680  
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556  
 45 C-PLACE1003454  
 C-PLACE1003478  
 C-PLACE1003516  
 C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136  
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//  
 50 Q09475  
 C-PLACE1003528  
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-  
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT).//7.7E-68//404aa//33%//P32802  
 55 C-PLACE1003566  
 C-PLACE1003584  
 C-PLACE1003593  
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL

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ACTIVATOR.//0.00000023//82aa//35%//Q02516  
 C-PLACE1003618  
 C-PLACE1003638  
 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742  
 5 C-PLACE1003760//&quot;Homo sapiens tetraspanin TM4-A mRNA, complete cds.&quot;//5.2E-289//1313bp//  
 97%//AF133423  
 C-PLACE1003768  
 C-PLACE1003795  
 C-PLACE1003886  
 10 C-PLACE1003888//&quot;Homo sapiens mRNA for KIAA1092 protein, partial cds.&quot;//0//2057bp//99%//  
 AB029015  
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//  
 584aa//74%//P17812  
 C-PLACE1003915//&quot;PROBABLE ARGINYLYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (AR-  
 15 GININE- -TRNA LIGASE) (ARGRS).&quot;//2.4E-108//581aa//40%//Q05506  
 C-PLACE1004118  
 C-PLACE1004256//&quot;Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.&quot;//  
 2E-93//960bp//76%//AF115778  
 C-PLACE1004274  
 20 C-PLACE1004284  
 C-PLACE1005331  
 C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//  
 99%//AL050267  
 C-PLACE1005828  
 25 C-PLACE1005876//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
 (CPSF 100 KD SUBUNIT).&quot;//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069  
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
 (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//  
 30 30%//P98110  
 C-PLACE1007053  
 C-PLACE1007068  
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652  
 C-PLACE1009921  
 35 C-PLACE1010401  
 C-PLACE1010856  
 C-PLACE1010857  
 C-PLACE1010917  
 C-PLACE1010925  
 40 C-PLACE1010926//&quot;Homo sapiens mRNA for KIAA0554 protein, partial cds.&quot;//0//1160bp//100%//  
 AB011126  
 C-PLACE1010942//&quot;Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.&quot;//0//1440bp//  
 99%//AF114487  
 C-PLACE1010944  
 45 C-PLACE1010954  
 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890  
 C-PLACE1011026  
 C-PLACE1011046//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1  
 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).&quot;//0//646aa//97%//P10894  
 50 C-PLACE1011054  
 C-PLACE1011057  
 C-PLACE1011109//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//1.50E-  
 22//63aa//88%//Q07803  
 C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532  
 55 C-PLACE1011133  
 C-PLACE1011143  
 C-PLACE1011165  
 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

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C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.-)//3.2E-12//212aa//29%//Q03326  
 C-PLACE1011221  
 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp564O043)//0//2487bp//  
 99%//AL050390  
 5 C-PLACE1011325  
 C-PLACE1011332//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//  
 7.2E-151//697bp//99%//AF102265  
 C-PLACE1011340//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//1.20E-74//380bp//97%//  
 AB019602  
 10 C-PLACE1011399//&quot;Homo sapiens CGI-72 protein mRNA, complete cds.&quot;//3.2E-90//427bp//99%//  
 AF151830  
 C-PLACE1011433//&quot;Homo sapiens mRNA for KIAA0530 protein, partial cds.&quot;//0//1946bp//99%//  
 AB011102  
 C-PLACE1011452  
 15 C-PLACE1011465  
 C-PLACE1011472//&quot;Homo sapiens mRNA for KIAA0712 protein, complete cds.&quot;//0//2022bp//99%//  
 AB018255  
 C-PLACE1011477//&quot;Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.&quot;//0//2040bp//99%//  
 AF065482  
 20 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//  
 4.90E-11//147aa//32%//P52178  
 C-PLACE1011520  
 C-PLACE1011563  
 C-PLACE1011567  
 25 C-PLACE1011576//&quot;Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.&quot;//0//  
 1791bp//82%//L11672  
 C-PLACE1011586  
 C-PLACE1011643  
 C-PLACE1011649  
 30 C-PLACE1011664//CROOKED NECK PROTEIN//1.6E-187//505aa//64%//P17886  
 C-PLACE1011682  
 C-PLACE1011719  
 C-PLACE1011729  
 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021)//0//1490bp//  
 35 99%//AL050287  
 C-PLACE1011874  
 C-PLACE1011875//&quot;Homo sapiens mRNA for KIAA0580 protein, partial cds.&quot;//4.1E-112//524bp//  
 100%//AB011152  
 C-PLACE1011923//&quot;Homo sapiens serum-inducible kinase mRNA, complete cds.&quot;//0//2782bp//99%//  
 40 AF059617  
 C-PLACE1011982  
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//2.6E-42//104aa//49%//  
 Q09475  
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 45 EPS15) (AF-1P PROTEIN)//1.1E-116//364aa//45%//P42566  
 C-PLACE2000017  
 C-PLACE2000021//&quot;Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, com-  
 plete cds.&quot;//2.7E-107//981bp//74%//AF082556  
 C-PLACE2000047  
 50 C-PLACE2000062//&quot;Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type  
 lectin, complete cds, clone:HP01347.&quot;//6.3E-166//656bp//94%//AB015629  
 C-PLACE2000100  
 C-PLACE2000111  
 C-PLACE2000172  
 55 C-PLACE2000187  
 C-PLACE2000216//&quot;Dog nonerythroid beta-spectrin mRNA, 3' end.&quot;//3.2E-253//1799bp//83%//L02897  
 C-PLACE2000246//&quot;Homo sapiens mRNA for KIAA0795 protein, partial cds.&quot;//4.60E-172//796bp//  
 99%//AB018338

C-PLACE2000317  
 C-PLACE2000341//&quot;Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete  
 cds.&quot;0//1554bp//99%//AF069307  
 C-PLACE2000366  
 5 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446  
 C-PLACE2000394  
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//  
 90aa//98%//P10586  
 C-PLACE2000411//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;0//2515bp//99%//  
 10 AB028960  
 C-PLACE2000425  
 C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333  
 C-PLACE2000433  
 C-PLACE2000438//&quot;POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-  
 15 TEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALAC-  
 TOSAMINYLTRANSFERASE)(GALNAC-T1).&quot;2.1E-86//348aa//41%//Q10472  
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25//  
 165aa//40%//P33450  
 C-PLACE2000477//&quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&quot;6.7E-  
 20 127//671bp//94%//AF072733  
 C-PLACE3000009  
 C-PLACE3000020//&quot;Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.&quot;0//  
 2253bp//99%//AF033861  
 C-PLACE3000103  
 25 C-PLACE3000142  
 C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205  
 C-PLACE3000156  
 C-PLACE3000157  
 C-PLACE3000197  
 30 C-PLACE3000208  
 C-PLACE3000226//&quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;0//4805bp//99%//  
 AB023179  
 C-PLACE3000242//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;0//2786bp//96%//  
 AB029037  
 35 C-PLACE3000363  
 C-PLACE3000405  
 C-PLACE3000416//&quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&quot;1.80E-  
 141//565bp//98%//AB029290  
 C-PLACE3000477  
 40 C-PLACE4000106//&quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&quot;0//6702bp//99%//  
 AB007931  
 C-PLACE4000323  
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT  
 SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771  
 45 C-PLACE4000369//&quot;Homo sapiens mRNA for KIAA1025 protein, partial cds.&quot;0//4830bp//99%//  
 AB028948  
 C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//  
 99%//AL080196  
 C-PLACE4000558//&quot;Homo sapiens mRNA for KIAA0729 protein, partial cds.&quot;0//1051bp//97%//  
 50 AB018272  
 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1)  
 (UEGF-1).//9.3E-70//226aa//52%//P10079  
 C-PLACE4000593  
 C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 55 (EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414  
 C-PLACE4000670  
 C-THYRO1000026  
 C-THYRO1000085//&quot;PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.&quot;2E-72//155aa//92%//

Q06710  
 C-THYRO1000107  
 C-THYRO1000111  
 5 C-THYRO1000132//&quot;Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.&quot;//1.1E-159//824bp//95%//U97018  
 C-THYRO1000156  
 C-THYRO1000173//&quot;Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.&quot;//0//1713bp//99%//AF020797  
 C-THYRO1000186  
 10 C-THYRO1000187  
 C-THYRO1000241  
 C-THYRO1000279  
 C-THYRO1000327//&quot;Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.&quot;//0//1567bp//99%//AF124145  
 15 C-THYRO1000452  
 C-THYRO1000471  
 C-THYRO1000484  
 C-THYRO1000502  
 C-THYRO1000505  
 20 C-THYRO1000585//&quot;Homo sapiens protein associated with Myc mRNA, complete cds.&quot;//0//1901bp//99%//AF075587  
 C-THYRO1000596  
 C-THYRO1000662//&quot;Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.&quot;//0//2341 bp//99%//AB024313  
 25 C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889  
 C-THYRO1000715  
 C-THYRO1000734  
 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171  
 30 C-THYRO1000756//&quot;ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).&quot;//1.8E-55//243aa//42%//Q64686  
 C-THYRO1000777  
 C-THYRO1000783//&quot;Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.&quot;//2.4E-157//1656bp//70%//U37373  
 35 C-THYRO1000787  
 C-THYRO1000793  
 C-THYRO1000796  
 C-THYRO1000843  
 C-THYRO1000852//&quot;Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds.&quot;//3.3E-147//790bp//93%//U68418  
 40 C-THYRO1000865  
 C-THYRO1000895  
 C-THYRO1000926//&quot;Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.&quot;//0//2387bp//99%//AF079529  
 45 C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550  
 C-THYRO1000952  
 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132  
 50 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491  
 C-THYRO1001031  
 C-THYRO1001062  
 C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168  
 55 C-THYRO1001133  
 C-THYRO1001134//&quot;Homo sapiens CGI-78 protein mRNA, complete cds.&quot;//0//1898bp//99%//AF151835  
 C-THYRO1001173



C-THYRO1001213  
 C-THYRO1001321  
 C-THYRO1001322  
 C-THYRO1001365  
 5 C-THYRO1001401  
 C-THYRO1001411  
 C-THYRO1001434  
 C-THYRO1001534  
 C-THYRO1001541  
 10 C-THYRO1001559  
 C-THYRO1001570  
 C-THYRO1001595  
 C-THYRO1001605  
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//  
 15 99%//AJ002190  
 C-THYRO1001656//&quot;Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.&quot;//4.1E-  
 273//1947bp//82%//AF175968  
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//  
 AJ225089  
 20 C-THYRO1001673  
 C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672  
 C-THYRO1001706  
 C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584  
 C-THYRO1001745  
 25 C-THYRO1001793  
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128  
 C-THYRO1001895  
 C-THYRO1001907  
 C-VESEN1000122  
 30 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916  
 C-Y79AA1000059//&quot;Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.&quot;//2.9E-70//  
 1040bp//65%//U78521  
 C-Y79AA1000065  
 C-Y79AA1000131  
 35 C-Y79AA1000181//&quot;Homo sapiens CGI-01 protein mRNA, complete cds.&quot;//0//1858bp//99%//  
 AF132936  
 C-Y79AA1000202  
 C-Y79AA1000214//&quot;Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.&quot;//7.1E-71//  
 345bp//100%//AF081192  
 40 C-Y79AA1000230  
 C-Y79AA1000258  
 C-Y79AA1000268//&quot;Mus musculus Nip21 mRNA, complete cds.&quot;//2.10E-50//648bp//64%//AF035207  
 C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910  
 C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25 %//Q93794  
 45 C-Y79AA1000355  
 C-Y79AA1000368//REDUCED VIABILTY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343  
 C-Y79AA1000420  
 C-Y79AA1000469//&quot;Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-  
 plete cds.&quot;//8.30E-252//1207bp//85%//U41736  
 50 C-Y79AA1000480  
 C-Y79AA1000540  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT).//0//652aa//98%//P17427  
 55 C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801  
 C-Y79AA1000627//&quot;Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.&quot;//2E-287//203  
 lbp//82%//AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

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C-Y79AA1000734//&quot;Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.&quot;//  
0//1594bp//99%//AF093670

C-Y79AA1000748//&quot;Homo sapiens CGI-05 protein mRNA, complete cds.&quot;//1.9E-239//1367bp//91%//  
AF152097

5 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
4.9E-91//200aa//64%//Q61990

C-Y79AA1000774

C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTEDASE (EC 3.1.3.5).//3E-37//469aa//27%//P49902

10 C-Y79AA1000784//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//1.10E-236//1076bp//  
99%//AF098799

C-Y79AA1000794//&quot;Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete  
cds.&quot;//0//1610bp//99%//AF105369

C-Y79AA1000800//&quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&quot;//1.6E-  
284//1288bp//99%//AF072733

15 C-Y79AA1000805

C-Y79AA1000824

C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209

C-Y79AA1000850

20 C-Y79AA1000962//&quot;MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).&quot;//  
4.2E-17//430aa//27%//Q99323

C-Y79AA1000968//&quot;Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, com-  
plete cds.&quot;//3.9E-248//1468bp//87%//U38253

C-Y79AA1000976

25 C-Y79AA1001023

C-Y79AA1001041

C-Y79AA1001048//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC  
1.3.99.-) (VLCAD).&quot;//3.1E-138//583aa//47%//P45953

C-Y79AA1001077

C-Y79AA1001078

30 C-Y79AA1001145

C-Y79AA1001177

C-Y79AA1001185

C-Y79AA1001211//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.&quot;//  
0//1435bp//99%//AF139658

35 C-Y79AA1001228

C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
DROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//P51657

C-Y79AA1001236//&quot;Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581  
and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).&quot;//0//1653bp//99%//AJ005892

40 C-Y79AA1001281

C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//  
Q03309

C-Y79AA1001323//&quot;Mus musculus mRNA for GSG1, complete cds.&quot;//3.3E-172//1171bp//83%//  
D87325

45 C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%//P31271

C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746

C-Y79AA1001402//&quot;Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.  
&quot;//8.50E-65//784bp//62%//AF083115

50 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132

C-Y79AA1001533//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//  
4.5E-193//1333bp//80%//D14336

C-Y79AA1001541

55 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
NASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356

C-Y79AA1001555

C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
TIVATING ENZYME).//1.9E-40//482aa//27%//P27550

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C-Y79AA1001585  
 C-Y79AA1001603//&quot;POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-  
 TEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALAC-  
 TOSAMINYLTRANSFERASE) (GALNAC-T1).&quot;//1.7E-84//313aa//48%//Q07537  
 5 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91//209aa//41%//P52740  
 C-Y79AA1001665  
 C-Y79AA1001679//&quot;Homo sapiens lambda-crystallin mRNA, complete cds.&quot;//3.4e-310//1430bp//98%//  
 AF077049  
 C-Y79AA1001696//&quot;Homo sapiens mRNA for KIAA1109 protein, partial cds.&quot;//0//1669bp//100%//  
 10 AB029032  
 C-Y79AA1001705//&quot;Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.  
 &quot;//3.4E-47//626bp//68%//AF033120  
 C-Y79AA1001711//&quot;Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.&quot;//1.2E-258//  
 1185bp//99%//J04137  
 15 C-Y79AA1001781  
 C-Y79AA1001805  
 C-Y79AA1001827//&quot;Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, com-  
 plete cds.&quot;//0//1689bp//98%//AF177145  
 C-Y79AA1001846  
 20 C-Y79AA1001923  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 SPAC10F6.02C.//1E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743  
 25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018  
 C-Y79AA1002089  
 C-Y79AA1002115  
 C-Y79AA1002125  
 C-Y79AA1002204  
 30 C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%//Q02357  
 C-Y79AA1002209//&quot;Homo sapiens CGI-04 protein mRNA, complete cds.&quot;//0//1617bp//99%//  
 AF132939  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620  
 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//32%//000445  
 35 C-Y79AA1002298  
 C-Y79AA1002307//&quot;Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.&quot;//0//1209bp//99%//  
 AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.9E-186//1130bp//82%//  
 X67877  
 40 C-Y79AA1002351  
 C-Y79AA1002407  
 C-Y79AA1002433//&quot;Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit  
 mRNA, complete cds.&quot;//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5E-136//472aa//  
 45 49%//Q05481

## Homology Search Result Data 13.

50 [0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
 es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,  
 and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//  
 55 AF196304  
 C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.50E-153//525bp//91%//Z70200  
 C-HEMBA1000213  
 C-HEMBA1000243

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C-HEMBA1000244  
 C-HEMBA1000251  
 C-HEMBA1000338  
 C-HEMBA1000357  
 5 C-HEMBA1000376  
 C-HEMBA1000428  
 C-HEMBA1000469  
 C-HEMBA1000497  
 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//  
 10 25%//Q05481  
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865  
 C-HEMBA1000575  
 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
 C-HEMBA1000673  
 15 C-HEMBA1000702  
 C-HEMBA1000722  
 C-HEMBA1000726  
 C-HEMBA1000876  
 C-HEMBA1000942  
 20 C-HEMBA1000943  
 C-HEMBA1000960  
 C-HEMBA1000985  
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)  
 (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
 25 C-HEMBA1001020  
 C-HEMBA1001024  
 C-HEMBA1001026  
 C-HEMBA1001051  
 C-HEMBA1001060  
 30 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461  
 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//  
 432bp//94%//AF119043  
 C-HEMBA1001099  
 C-HEMBA1001121  
 35 C-HEMBA1001123  
 C-HEMBA1001208  
 C-HEMBA1001213  
 C-HEMBA1001226  
 C-HEMBA1001247  
 40 C-HEMBA1001299  
 C-HEMBA1001319  
 C-HEMBA1001323  
 C-HEMBA1001327  
 C-HEMBA1001361  
 45 C-HEMBA1001375  
 C-HEMBA1001377  
 C-HEMBA1001383  
 C-HEMBA1001391  
 C-HEMBA1001411  
 50 C-HEMBA1001432  
 C-HEMBA1001433  
 C-HEMBA1001435  
 C-HEMBA1001442  
 C-HEMBA1001463  
 55 C-HEMBA1001515  
 C-HEMBA1001522  
 C-HEMBA1001557  
 C-HEMBA1001566

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C-HEMBA1001589  
 C-HEMBA1001608  
 C-HEMBA1001636  
 C-HEMBA1001647  
 5 C-HEMBA1001651  
 C-HEMBA1001658  
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//  
 P54787  
 C-HEMBA1001712  
 10 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//  
 1.10E-38//87aa//96%//P55288  
 C-HEMBA1001745  
 C-HEMBA1001750  
 C-HEMBA1001784  
 15 C-HEMBA1001791  
 C-HEMBA1001803  
 C-HEMBA1001820  
 C-HEMBA1001835  
 C-HEMBA1001888  
 20 C-HEMBA1001912  
 C-HEMBA1001915  
 C-HEMBA1001918  
 C-HEMBA1001940  
 C-HEMBA1001942  
 25 C-HEMBA1001964  
 C-HEMBA1002022  
 C-HEMBA1002039  
 C-HEMBA1002100  
 C-HEMBA1002113  
 30 C-HEMBA1002119  
 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
 C-HEMBA1002160  
 C-HEMBA1002162  
 C-HEMBA1002166  
 35 C-HEMBA1002185  
 C-HEMBA1002204  
 C-HEMBA1002328  
 C-HEMBA1002337  
 C-HEMBA1002348  
 40 C-HEMBA1002381  
 C-HEMBA1002486  
 C-HEMBA1002498  
 C-HEMBA1002538  
 C-HEMBA1002552  
 45 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//  
 68%//AF055993  
 C-HEMBA1002558  
 C-HEMBA1002621  
 C-HEMBA1002629  
 50 C-HEMBA1002645  
 C-HEMBA1002659  
 C-HEMBA1002661  
 C-HEMBA1002666  
 C-HEMBA1002678  
 55 C-HEMBA1002679  
 C-HEMBA1002712  
 C-HEMBA1002716  
 C-HEMBA1002742

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C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746  
 C-HEMBA1002748  
 C-HEMBA1002780  
 C-HEMBA1002801  
 5 C-HEMBA1002826  
 C-HEMBA1002833  
 C-HEMBA1002921  
 C-HEMBA1002934  
 C-HEMBA1002944  
 10 C-HEMBA1002968  
 C-HEMBA1003034  
 C-HEMBA1003037  
 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858  
 15 C-HEMBA1003078  
 C-HEMBA1003083  
 C-HEMBA1003086  
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096  
 C-HEMBA1003133  
 20 C-HEMBA1003142  
 C-HEMBA1003166  
 C-HEMBA1003197  
 C-HEMBA1003202  
 C-HEMBA1003220  
 25 C-HEMBA1003229  
 C-HEMBA1003276  
 C-HEMBA1003278  
 C-HEMBA1003328  
 C-HEMBA1003373  
 30 C-HEMBA1003597  
 C-HEMBA1003598  
 C-HEMBA1003656  
 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//  
 423aa//47%//P34629  
 35 C-HEMBA1003733  
 C-HEMBA1003742  
 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665  
 C-HEMBA1003803  
 40 C-HEMBA1003854  
 C-HEMBA1003926  
 C-HEMBA1003939  
 C-HEMBA1003987  
 C-HEMBA1004012  
 45 C-HEMBA1004015  
 C-HEMBA1004193  
 C-HEMBA1004225  
 C-HEMBA1004241  
 C-HEMBA1004267  
 50 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103  
 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516  
 C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494  
 C-HEMBA1004396  
 C-HEMBA1004405  
 55 C-HEMBA1004433  
 C-HEMBA1004538  
 C-HEMBA1004542  
 C-HEMBA1004573

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C-HEMBA1004577  
 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844  
 C-HEMBA1004617  
 C-HEMBA1004631  
 5 C-HEMBA1004705  
 C-HEMBA1004733  
 C-HEMBA1004748  
 C-HEMBA1004778  
 C-HEMBA1004803  
 10 C-HEMBA1004807  
 C-HEMBA1004820  
 C-HEMBA1004865  
 C-HEMBA1004880  
 C-HEMBA1004900  
 15 C-HEMBA1004909  
 C-HEMBA1004960  
 C-HEMBA1004978  
 C-HEMBA1004980  
 C-HEMBA1004983  
 20 C-HEMBA1004995  
 C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548  
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947  
 C-HEMBA1005035  
 C-HEMBA1005039  
 25 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290  
 C-HEMBA1005050  
 C-HEMBA1005062  
 C-HEMBA1005066  
 C-HEMBA1005075  
 30 C-HEMBA1005079  
 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//  
 AF080561  
 C-HEMBA1005123  
 C-HEMBA1005149  
 35 C-HEMBA1005152  
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941  
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//  
 Q00004  
 C-HEMBA1005223  
 40 C-HEMBA1005232  
 C-HEMBA1005241  
 C-HEMBA1005275  
 C-HEMBA1005293  
 C-HEMBA1005311  
 45 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581  
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743  
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//  
 AF071787  
 C-HEMBA1005374  
 50 C-HEMBA1005382  
 C-HEMBA1005411  
 C-HEMBA1005426  
 C-HEMBA1005443  
 C-HEMBA1005447  
 55 C-HEMBA1005497  
 C-HEMBA1005500  
 C-HEMBA1005506  
 C-HEMBA1005508

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C-HEMBA1005526  
C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//  
1578bp//98%//AF191340  
5 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,  
complete cds.//1.00E-220//1014bp//99%//AF134157  
C-HEMBA1005552  
C-HEMBA1005568  
C-HEMBA1005588  
C-HEMBA1005593  
10 C-HEMBA1005606  
C-HEMBA1005616  
C-HEMBA1005627  
C-HEMBA1005670  
C-HEMBA1005679  
15 C-HEMBA1005699  
C-HEMBA1005705  
C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697  
C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEU-  
TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789  
20 C-HEMBA1005852  
C-HEMBA1005894  
C-HEMBA1005921  
C-HEMBA1006035  
C-HEMBA1006036  
25 C-HEMBA1006090  
C-HEMBA1006138  
C-HEMBA1006173  
C-HEMBA1006252  
C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836  
30 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193  
C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160  
C-HEMBA1006380  
C-HEMBA1006416  
C-HEMBA1006421  
35 C-HEMBA1006424  
C-HEMBA1006426  
C-HEMBA1006446  
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//  
97%//P55786  
40 C-HEMBA1006486  
C-HEMBA1006494  
C-HEMBA1006546  
C-HEMBA1006562  
C-HEMBA1006595  
45 C-HEMBA1006597  
C-HEMBA1006631  
C-HEMBA1006639  
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
C-HEMBA1006659  
50 C-HEMBA1006665  
C-HEMBA1006676  
C-HEMBA1006695  
C-HEMBA1006709  
55 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//  
91%//AF152492  
C-HEMBA1006780  
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644  
C-HEMBA1006824



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C-HEMBA1006865  
C-HEMBA1006921  
C-HEMBA1006949  
C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//  
5 447bp//89%//X74570  
C-HEMBA1007051  
C-HEMBA1007052  
C-HEMBA1007066  
C-HEMBA1007073  
10 C-HEMBA1007078  
C-HEMBA1007085  
C-HEMBA1007113  
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//  
92%//AF125042  
15 C-HEMBA1007129  
C-HEMBA1007147  
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929  
C-HEMBA1007178  
C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%//D86987  
20 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//  
AF196304  
C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060  
C-HEMBA1007251  
C-HEMBA1007288  
25 C-HEMBA1007322  
C-HEMBA1007341  
C-HEMBA1000050  
C-HEMBA1000054  
C-HEMBA1000059  
30 C-HEMBA1000089  
C-HEMBA1000113  
C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE  
ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177  
C-HEMBA1000173  
35 C-HEMBA1000175  
C-HEMBA1000272  
C-HEMBA1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888  
C-HEMBA1000318  
C-HEMBA1000336  
40 C-HEMBA1000341  
C-HEMBA1000343  
C-HEMBA1000354  
C-HEMBA1000374  
C-HEMBA1000434  
45 C-HEMBA1000441  
C-HEMBA1000491  
C-HEMBA1000493  
C-HEMBA1000510  
C-HEMBA1000652  
50 C-HEMBA1000672  
C-HEMBA1000684  
C-HEMBA1000709  
C-HEMBA1000726  
C-HEMBA1000770  
55 C-HEMBA1000827  
C-HEMBA1000831  
C-HEMBA1000883  
C-HEMBA1000888

C-HEMBB1000893  
 C-HEMBB1000913  
 C-HEMBB1000996  
 C-HEMBB1001004  
 5 C-HEMBB1001047  
 C-HEMBB1001060  
 C-HEMBB1001114  
 C-HEMBB1001119  
 C-HEMBB1001133  
 10 C-HEMBB1001142  
 C-HEMBB1001177  
 C-HEMBB1001208  
 C-HEMBB1001209  
 C-HEMBB1001249  
 15 C-HEMBB1001253  
 C-HEMBB1001254  
 C-HEMBB1001271  
 C-HEMBB1001304  
 C-HEMBB1001317  
 20 C-HEMBB1001348  
 C-HEMBB1001394  
 C-HEMBB1001410  
 C-HEMBB1001424  
 C-HEMBB1001426  
 25 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001436  
 C-HEMBB10014437//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 C-HEMBB1001449  
 30 C-HEMBB1001458  
 C-HEMBB1001521  
 C-HEMBB1001531  
 C-HEMBB1001535  
 C-HEMBB1001536  
 35 C-HEMBB1001564  
 C-HEMBB1001565  
 C-HEMBB1001585  
 C-HEMBB1001588  
 C-HEMBB1001603  
 40 C-HEMBB1001618  
 C-HEMBB1001635  
 C-HEMBB1001653  
 C-HEMBB1001668  
 C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546  
 45 C-HEMBB1001685  
 C-HEMBB1001695  
 C-HEMBB1001707  
 C-HEMBB1001735  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 50 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001747  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001753  
 C-HEMBB1001756  
 55 C-HEMBB1001760  
 C-HEMBB1001785  
 C-HEMBB1001797  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

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C-HEMBB1001816  
 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLGCF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 5 P18720  
 C-HEMBB1001850  
 C-HEMBB1001863  
 C-HEMBB1001868  
 C-HEMBB1001874  
 10 C-HEMBB1001880  
 C-HEMBB1001899  
 C-HEMBB1001906  
 C-HEMBB1001910  
 C-HEMBB1001911  
 15 C-HEMBB1001921  
 C-HEMBB1001922  
 C-HEMBB1001930  
 C-HEMBB1001944  
 C-HEMBB1001945  
 20 C-HEMBB1001947  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)  
 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1001952  
 C-HEMBB1001957  
 25 C-HEMBB1001962  
 C-HEMBB1001983  
 C-HEMBB1001990  
 C-HEMBB1001996  
 C-HEMBB1002002  
 30 C-HEMBB1002005  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002043  
 C-HEMBB1002045  
 C-HEMBB1002049  
 35 C-HEMBB1002050  
 C-HEMBB1002068  
 C-HEMBB1002092  
 C-HEMBB1002139  
 C-HEMBB1002142  
 40 C-HEMBB1002190  
 C-HEMBB1002193  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002218  
 45 C-HEMBB1002232  
 C-HEMBB1002247  
 C-HEMBB1002249  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002327  
 50 C-HEMBB1002329  
 C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//  
 AJ010841  
 C-HEMBB1002358  
 C-HEMBB1002371  
 55 C-HEMBB1002387  
 C-HEMBB1002409  
 C-HEMBB1002425  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

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C-HEMBB1002453  
 C-HEMBB1002458  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002489  
 5 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002520  
 C-HEMBB1002522  
 C-HEMBB1002545  
 C-HEMBB1002579  
 10 C-HEMBB1002582  
 C-HEMBB1002596  
 C-HEMBB1002603  
 C-HEMBB1002610  
 C-HEMBB1002613  
 15 C-HEMBB1002617  
 C-HEMBB1002623  
 C-HEMBB1002635  
 C-HEMBB1002677  
 C-HEMBB1002683  
 20 C-HEMBB1002699  
 C-HEMBB1002702  
 C-MAMMA1000009  
 C-MAMMA1000043  
 25 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000057  
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000092  
 30 C-MAMMA1000103  
 C-MAMMA1000117  
 C-MAMMA1000129  
 C-MAMMA1000133  
 C-MAMMA1000155  
 35 C-MAMMA1000175  
 C-MAMMA1000198  
 C-MAMMA1000241  
 C-MAMMA1000251  
 C-MAMMA1000254  
 40 C-MAMMA1000287  
 C-MAMMA1000307  
 C-MAMMA1000331  
 C-MAMMA1000339  
 C-MAMMA1000340  
 45 C-MAMMA1000348  
 C-MAMMA1000356  
 C-MAMMA1000360  
 C-MAMMA1000402  
 C-MAMMA1000414  
 50 C-MAMMA1000431  
 C-MAMMA1000444  
 C-MAMMA1000458  
 C-MAMMA1000500  
 C-MAMMA1000522  
 55 C-MAMMA1000576  
 C-MAMMA1000583  
 C-MAMMA1000594  
 C-MAMMA1000605

C-MAMMA1000616  
 C-MAMMA1000643  
 C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134  
 C-MAMMA1000696  
 5 C-MAMMA1000707  
 C-MAMMA1000714  
 C-MAMMA1000720  
 C-MAMMA1000744  
 C-MAMMA1000761  
 10 C-MAMMA1000776  
 C-MAMMA1000798  
 C-MAMMA1000839  
 C-MAMMA1000851  
 C-MAMMA1000863  
 15 C-MAMMA1000867  
 C-MAMMA1000876  
 C-MAMMA1000880  
 C-MAMMA1000883  
 C-MAMMA1000921  
 20 C-MAMMA1000931  
 C-MAMMA1000941  
 C-MAMMA1000957  
 C-MAMMA1000962  
 C-MAMMA1000975  
 25 C-MAMMA1000987  
 C-MAMMA1001003  
 C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)  
 (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674  
 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 30 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746  
 C-MAMMA1001082  
 C-MAMMA1001162  
 C-MAMMA1001186  
 C-MAMMA1001191  
 35 C-MAMMA1001206  
 C-MAMMA1001220  
 C-MAMMA1001243  
 C-MAMMA1001249  
 C-MAMMA1001256  
 40 C-MAMMA1001268  
 C-MAMMA1001271  
 C-MAMMA1001274  
 C-MAMMA1001292  
 C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)  
 45 (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)  
 (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960  
 C-MAMMA1001324  
 C-MAMMA1001341  
 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750  
 50 C-MAMMA1001397  
 C-MAMMA1001408  
 C-MAMMA1001420  
 C-MAMMA1001442  
 C-MAMMA1001452  
 55 C-MAMMA1001465  
 C-MAMMA1001487  
 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

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C-MAMMA1001547  
 C-MAMMA1001551  
 C-MAMMA1001575  
 C-MAMMA1001590  
 5 C-MAMMA1001600  
 C-MAMMA1001606  
 C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989  
 C-MAMMA1001663  
 C-MAMMA1001670  
 10 C-MAMMA1001671  
 C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
 C-MAMMA1001711  
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
 C-MAMMA1001744  
 15 C-MAMMA1001745  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete  
 cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001783  
 C-MAMMA1001788  
 20 C-MAMMA1001806  
 C-MAMMA1001812  
 C-MAMMA1001815  
 C-MAMMA1001817  
 C-MAMMA1001818  
 25 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 C-MAMMA1001824  
 C-MAMMA1001851  
 C-MAMMA1001854  
 C-MAMMA1001864  
 30 C-MAMMA1001878  
 C-MAMMA1001890  
 C-MAMMA1001907  
 C-MAMMA1001908  
 C-MAMMA1001931  
 35 C-MAMMA1001969  
 C-MAMMA1002011  
 C-MAMMA1002032  
 C-MAMMA1002041  
 C-MAMMA1002047  
 40 C-MAMMA1002056  
 C-MAMMA1002058  
 C-MAMMA1002078  
 C-MAMMA1002082  
 C-MAMMA1002084  
 45 C-MAMMA1002093  
 C-MAMMA1002094  
 C-MAMMA1002118  
 C-MAMMA1002125  
 C-MAMMA1002132  
 50 C-MAMMA1002140  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds7//1.70E-252//1170bp//99%//  
 AF099664  
 C-MAMMA1002145  
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE  
 55 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR  
 B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002230  
 C-MAMMA1002250

C-MAMMA1002282  
 C-MAMMA1002293  
 C-MAMMA1002298  
 C-MAMMA1002299  
 5 C-MAMMA1002308  
 C-MAMMA1002310  
 C-MAMMA1002311  
 C-MAMMA1002322  
 C-MAMMA1002339  
 10 C-MAMMA1002352  
 C-MAMMA1002359  
 C-MAMMA1002360  
 C-MAMMA1002392  
 C-MAMMA1002411  
 15 C-MAMMA1002413  
 C-MAMMA1002417  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE  
 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 C-MAMMA1002434  
 20 C-MAMMA1002446  
 C-MAMMA1002454  
 C-MAMMA1002461  
 C-MAMMA1002475  
 C-MAMMA1002556  
 25 C-MAMMA1002566  
 C-MAMMA1002612  
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 30 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//  
 1942bp//85%//AF018261  
 C-MAMMA1002727  
 C-MAMMA1002748  
 C-MAMMA1002758  
 35 C-MAMMA1002780  
 C-MAMMA1002820  
 C-MAMMA1002833  
 C-MAMMA1002843  
 C-MAMMA1002895  
 40 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
 C-MAMMA1003004  
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//  
 1533bp//99%//AF077952  
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110  
 45 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886  
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590  
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775 C-NT2RM1000499  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//  
 50 Q99383  
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//  
 52%//Q05481  
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990  
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518  
 55 C-NT2RM2001637  
 C-NT2RM2001641  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001699

C-NT2RM2001706  
 C-NT2RM2001718  
 C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931  
 C-NT2RM2001805  
 5 C-NT2RM4000086  
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962  
 C-NT2RM4000414  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000634  
 10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%//AB028992  
 C-NT2RM4000783  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000971  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//  
 15 50%//Q05481  
 C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532  
 C-NT2RM4001569  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
 20 8.10E-300//1395bp//98%//M37712  
 C-NT2RM4001905  
 C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%//AB020705  
 C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//  
 1.90E-31//80aa//52%//P36419  
 25 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//  
 AF072758  
 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//  
 2550bp//99%//AF176085  
 C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%//  
 30 AF071592  
 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940  
 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430  
 C-NT2RM4002390  
 C-NT2RM4002398  
 35 C-NT2RM4002420  
 C-NT2RM4002534  
 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962  
 C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//  
 4.60E-78//921bp//69%//X85019  
 40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//  
 88%//AL050019  
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//8.20E-83//345aa//47%//Q61068  
 45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//  
 99%//AL050118  
 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
 PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
 50 1687bp//99%//AF145020  
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//  
 98%//AF047020  
 C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094  
 C-NT2RP1000916  
 55 C-NT2RP1000944  
 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//  
 U82267  
 C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218



C-NT2RP1001113  
 C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%//AL080222  
 C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139  
 5 C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192  
 C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513  
 10 C-NT2RP1001311  
 C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799  
 C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034  
 C-NT2RP2000027  
 15 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675  
 C-NT2RP2000198  
 C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238  
 20 C-NT2RP2000551  
 C-NT2RP2000644  
 C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955  
 C-NT2RP2000678  
 C-NT2RP2000715  
 25 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811  
 C-NT2RP2000970  
 C-NT2RP2001347  
 C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709  
 30 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391  
 C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067  
 C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%//AF058718  
 35 C-NT2RP2001677  
 C-NT2RP2001678  
 C-NT2RP2001720  
 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068  
 40 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523  
 C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009  
 C-NT2RP2001861  
 45 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754  
 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008  
 C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161  
 50 C-NT2RP2001936  
 C-NT2RP2001943  
 C-NT2RP2001946  
 C-NT2RP2002032  
 C-NT2RP2002033  
 55 C-NT2RP2002041  
 C-NT2RP2002047  
 C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

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C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020  
 C-NT2RP2002172  
 C-NT2RP2002219  
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418  
 5 C-NT2RP2002316  
 C-NT2RP2002373  
 C-NT2RP2002439  
 C-NT2RP2002475  
 C-NT2RP2002546  
 10 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
 C-NT2RP2002643  
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
 15 C-NT2RP2002736  
 C-NT2RP2002740  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
 C-NT2RP2002752  
 C-NT2RP2002753  
 20 C-NT2RP2002857  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%//Q13829  
 C-NT2RP2003073  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
 25 C-NT2RP2003206  
 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794  
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657  
 C-NT2RP2003237  
 30 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2003280  
 C-NT2RP2003293  
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386  
 35 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//O61068  
 C-NT2RP2003456  
 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783  
 40 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158  
 C-NT2RP2003559  
 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-59//270aa//46%//P19474  
 45 C-NT2RP2003581  
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215  
 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786  
 50 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637  
 C-NT2RP2003727  
 C-NT2RP2003751  
 55 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201  
 C-NT2RP2003825  
 C-NT2RP2003871

C-NT2RP2003885  
 C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%/P51954  
 C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%/AB007916  
 5 C-NT2RP2003988  
 C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//2.30E-53//141aa//78%/P20290  
 C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%/Q01513  
 10 C-NT2RP2004142  
 C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%/Y12781  
 C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%/AF003998  
 C-NT2RP2004207  
 15 C-NT2RP2004226  
 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%/AB015982  
 C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//427aa//26%/P19246  
 20 C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%/P32857  
 C-NT2RP2004321  
 C-NT2RP2004339  
 C-NT2RP2004347  
 C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//99%/AB028069  
 25 C-NT2RP2004399  
 C-NT2RP2004400  
 C-NT2RP2004412  
 C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%/AF155739  
 30 C-NT2RP2004490  
 C-NT2RP2004523  
 C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%/AF090190  
 C-NT2RP2004580  
 35 C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%/AB020695  
 C-NT2RP2004594  
 C-NT2RP2004681  
 C-NT2RP2004709  
 C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%/AB023231  
 40 C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%/AB020691  
 C-NT2RP2004767  
 C-NT2RP2004775  
 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-228//1666bp//75%/U56732  
 45 C-NT2RP2004962  
 C-NT2RP2004982  
 C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//1.80E-99//376aa//43%/P19474  
 C-NT2RP2005018  
 50 C-NT2RP2005020  
 C-NT2RP2005022  
 C-NT2RP2005031  
 C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0//4069bp//99%/AB014564  
 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%/Q05921  
 55 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%/AJ007509  
 C-NT2RP2005254  
 C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

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99%//AF124735  
 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709  
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//  
 38%//P32660  
 5 C-NT2RP2005360  
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059  
 C-NT2RP2005454  
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete  
 cds.//1.20E-130//608bp//99%//AF070652  
 10 C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032  
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418  
 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742  
 C-NT2RP2005501  
 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171  
 15 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943  
 C-NT2RP2005645  
 C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//  
 Q92834  
 C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158  
 20 C-NT2RP2005741  
 C-NT2RP2005806  
 C-NT2RP2005815  
 C-NT2RP2005841  
 C-NT2RP2005882  
 25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
 FERASE).//1.50E-67//388aa//44%//P25500  
 C-NT2RP2006103  
 C-NT2RP2006166  
 C-NT2RP2006258  
 30 C-NT2RP2006261  
 C-NT2RP2006321  
 C-NT2RP2006454  
 C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//  
 1193bp//99%//AF113538  
 35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559  
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755  
 C-NT2RP3000418  
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-  
 1511319aa//26%//P37908  
 40 C-NT2RP3000487  
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667  
 C-NT2RP3000526  
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562  
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265  
 45 C-NT2RP3000628  
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//  
 155aa//37%//Q10149  
 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.).//8.30E-108//331aa//  
 50 50%//P27448  
 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027  
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//  
 54%//Q05481  
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//  
 P25386  
 55 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140  
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//  
 23%//P32380  
 C-NT2RP3001356

- C-NT2RP3001383  
 C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538  
 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821
- 5 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534  
 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177  
 C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554
- 10 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141  
 C-NT2RP3001739  
 C-NT2RP3001777  
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575
- 15 C-NT2RP3001944  
 C-NT2RP3002033  
 C-NT2RP3002054  
 C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956  
 C-NT2RP3002099  
 C-NT2RP3002102  
 C-NT2RP3002147  
 C-NT2RP3002163  
 C-NT2RP3002173  
 C-NT2RP3002255
- 25 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767  
 C-NT2RP3002343  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
- 30 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-79//416aa//34%//P33991  
 C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578  
 C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//99%//AL050092
- 35 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010  
 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598  
 C-NT2RP3002603
- 40 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660  
 C-NT2RP3002659  
 C-NT2RP3002660  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
- 45 C-NT2RP3002687  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002701  
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371  
 C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430
- 50 C-NT2RP3002876  
 C-NT2RP3002877  
 C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314  
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053  
 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333
- 55 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555  
 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357  
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

C-NT2RP3003078  
 C-NT2RP3003139  
 C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//  
 AF07773 8  
 5 C-NT2RP3003150  
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//  
 31%//Q09674  
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-  
 210//1851bp//76%//AF110267  
 10 C-NT2RP3003210  
 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-  
 187//1750bp//75%//U20286  
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656  
 C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//  
 15 AF098462  
 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 4.20E-86//366aa//48%//P19474  
 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//  
 585aa//54%//064948  
 20 C-NT2RP3003311  
 C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//  
 782bp//65%//U90653  
 C-NT2RP3003427  
 C-NT2RP3003543  
 25 C-NT2RP3003552  
 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//  
 191aa//40%//P40529  
 C-NT2RP3003564  
 C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//  
 30 AF106681  
 C-NT2RP3003621  
 C-NT2RP3003625  
 C-NT2RP3003656  
 C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843  
 35 C-NT2RP3003686  
 C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446  
 C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014  
 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//  
 U28164  
 40 C-NT2RP3003795  
 C-NT2RP3003805  
 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590  
 C-NT2RP3003819  
 C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//  
 45 P02720  
 C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete  
 cds.//2.2e-316//1436bp//99%//AB020523  
 C-NT2RP3003833  
 C-NT2RP3003842  
 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//  
 AB019435  
 C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343  
 C-NT2RP3003876  
 C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 55 (DUGT).//2.20E-20//76aa//64%//Q09332  
 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//  
 AF086628  
 C-NT2RP3003989

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C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)  
(KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263

C-NT2RP3004070

C-NT2RP3004145

5 C-NT2RP3004215

C-NT2RP3004253

C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871

C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//X67877

10 C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982

C-NT2RP3004503

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523

C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679

15 C-NT2RP4000023

C-NT2RP4000218

C-NT2RP4000424

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676

20 C-NT2RP4001447

C-NT2RP4001841

C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194

C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618

C-NT2RP4002075

25 C-NT2RP4002083

C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290

C-OVARC1000008

C-OVARC1000017

30 C-OVARC1000058

C-OVARC1000068

C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957

C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761

35 C-OVARC1000109

C-OVARC1000114

C-OVARC1000145

C-OVARC1000240

C-OVARC1000302

40 C-OVARC1000408

C-OVARC1000414

C-OVARC1000440

C-OVARC1000442

C-OVARC1000496

45 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349

C-OVARC1000557

C-OVARC1000578

C-OVARC1000622

50 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888

C-OVARC1000681

C-OVARC1000700

C-OVARC1000724

C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%//P49596

55 C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501

C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

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C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37)//0.0000054//135aa//28%/P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6//4.90E-10//61aaa//49%/P32943  
 C-OVARC1000960  
 C-OVARC1000971  
 5 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR//4.10E-11//189aa//32%/Q06527  
 C-OVARC1001000  
 C-OVARC1001029  
 C-OVARC1001040  
 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 10 EPS15) (AF-1P PROTEIN)//1.10E-08//216aa//23%/P42566  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//5.1e-310//1588bp//93%/AF051782  
 C-OVARC1001118  
 C-OVARC1001129  
 15 C-OVARC1001169  
 C-OVARC1001240  
 C-OVARC1001261  
 C-OVARC1001339  
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8//1.40E-110//207aa//99%/P09058  
 20 C-OVARC1001357  
 C-OVARC1001442  
 C-OVARC1001611  
 C-OVARC1001813  
 C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//0//1760bp//99%/AF054174  
 25 C-OVARC1002143  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2)//7.60E-08//114aa//37%/P31213  
 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP)//1.70E-  
 09//207aa//30%/Q91854  
 30 C-PLACE1000014  
 C-PLACE1000078  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds//0//2041bp//87%/U35245  
 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN//1.70E-07//251aa//24%/P23645  
 35 C-PLACE1000814  
 C-PLACE1000979//ZINC FINGER PROTEIN 135//2.50E-153//326aa//64%/P52742  
 C-PLACE1001007  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds//4.00E-300//  
 1355bp//100%/AB024301  
 40 C-PLACE1001088  
 C-PLACE1001136  
 C-PLACE1001241  
 C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//5.90E-228//827bp//99%/AF009615  
 45 C-PLACE1001395  
 C-PLACE1001740  
 C-PLACE1001746  
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION//7.50E-16//  
 319aa//26%/P37908  
 50 C-PLACE1002066  
 C-PLACE1002115  
 C-PLACE1002213  
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//0//1657bp//98%/AB018271  
 C-PLACE1002450//Human zinc finger protein mRNA, complete cds//0//2565bp//99%/U69274  
 55 C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds//0//2092bp//84%/U69262  
 C-PLACE1002499  
 C-PLACE1002578  
 C-PLACE1002714



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C-PLACE1002772  
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201  
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//  
 P51522  
 5 C-PLACE1002993  
 C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds.//8.50E-44//225bp//100%//AF032387  
 C-PLACE1003205  
 C-PLACE1003249  
 10 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481  
 C-PLACE1003553  
 C-PLACE1003592  
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//  
 P46975  
 15 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793  
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//  
 1316bp//98%//AF053305  
 C-PLACE1003870  
 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
 20 FERASE).//3.70E-222//651aa//66%//P25500  
 C-PLACE1003892  
 C-PLACE1003900  
 C-PLACE1004336  
 C-PLACE1004384  
 25 C-PLACE1004425  
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%//  
 P51522  
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-  
 16//402bp//62%//U90878  
 30 C-PLACE1004518  
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954  
 C-PLACE1004681  
 C-PLACE1004693  
 C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099  
 35 C-PLACE1004815  
 C-PLACE1004836  
 C-PLACE1004838  
 C-PLACE1004840  
 C-PLACE1004900  
 40 C-PLACE1004985  
 C-PLACE1005085  
 C-PLACE1005086  
 C-PLACE1005108  
 C-PLACE1005146  
 45 C-PLACE1005409  
 C-PLACE1005453  
 C-PLACE1005477  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005595  
 50 C-PLACE1005603  
 C-PLACE1005639  
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//  
 AF162680  
 C-PLACE1005799  
 55 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 C-PLACE1005884  
 C-PLACE1005968  
 C-PLACE1006002

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C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852  
 C-PLACE1006017  
 C-PLACE1006037  
 C-PLACE1006076  
 5 C-PLACE1006143  
 C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548  
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
 LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//  
 4.60E-117//147aa//80%//P21796  
 10 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374  
 C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 1.30E-18//460aa//24%//Q00547  
 C-PLACE1006371  
 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 15 TIVATING ENZYME).//1.20E-83//313aa//49%//P27550  
 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//  
 2170bp//99%//AF191338  
 C-PLACE1006521  
 C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//  
 20 883bp//99%//AL110144  
 C-PLACE1006617  
 C-PLACE1006640  
 C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//  
 6.20E-63//191aa//43%//P13688  
 25 C-PLACE1006760  
 C-PLACE1006779  
 C-PLACE1006805  
 C-PLACE1006815  
 C-PLACE1006867  
 30 C-PLACE1007045  
 C-PLACE1007097  
 C-PLACE1007111  
 C-PLACE1007112  
 C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226  
 35 C-PLACE1007218  
 C-PLACE1007454  
 C-PLACE1007478  
 C-PLACE1007677  
 C-PLACE10077057//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//  
 40 82%//AB033922  
 C-PLACE1007737  
 C-PLACE1007743  
 C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//  
 AB020685  
 45 C-PLACE1007877  
 C-PLACE1008045  
 C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326  
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
 50 C-PLACE1008231  
 C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-  
 TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315  
 C-PLACE1008331  
 55 C-PLACE1008369  
 C-PLACE1008392  
 C-PLACE1008405  
 C-PLACE1008424

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C-PLACE1008584  
 C-PLACE1008625  
 C-PLACE1008630  
 5 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//5.20E-90//483aa//38%//002668  
 C-PLACE1008715  
 C-PLACE1008748  
 C-PLACE1008757  
 C-PLACE1008798  
 10 C-PLACE1008851  
 C-PLACE1008947  
 C-PLACE1009039  
 C-PLACE1009048  
 C-PLACE1009050  
 15 C-PLACE10091137//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586  
 C-PLACE1009150  
 C-PLACE1009200  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 20 C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//AF191298  
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742  
 C-PLACE1009410  
 25 C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584  
 C-PLACE1009493  
 C-PLACE1009539  
 C-PLACE1009595  
 C-PLACE1009637  
 30 C-PLACE1009639  
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552  
 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%//P43510  
 C-PLACE1009888  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963  
 C-PLACE1009947  
 C-PLACE1010069  
 C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020  
 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//28%//Q14246  
 40 C-PLACE1010270  
 C-PLACE1010562  
 C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//1362bp//99%//AF200715  
 45 C-PLACE1010624  
 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907  
 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332  
 50 C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160  
 C-PLACE1010761  
 C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209  
 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580  
 55 C-PLACE1010916  
 C-PLACE1010947  
 C-PLACE1010965  
 C-PLACE1011032

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C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019  
C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//99%//AL050159  
5 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
C-PLACE1011214  
C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604  
C-PLACE1011273  
10 C-PLACE1011291  
C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703  
C-PLACE1011503  
15 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377  
C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752  
C-PLACE1011650  
C-PLACE1011675  
20 C-PLACE1011725  
C-PLACE1011749  
C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256  
25 C-PLACE2000006  
C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720  
C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586  
C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-291//1167bp//89%//L08505  
30 C-PLACE2000061  
C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219  
C-PLACE2000097  
C-PLACE2000103  
35 C-PLACE2000115  
C-PLACE2000124  
C-PLACE2000140  
C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736  
C-PLACE2000176  
40 C-PLACE2000223  
C-PLACE2000235  
C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098  
C-PLACE2000302  
C-PLACE2000347  
45 C-PLACE2000359  
C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205  
C-PLACE2000379  
C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209  
50 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996  
C-PLACE2000450  
C-PLACE2000455  
C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267  
55 C-PLACE3000070  
C-PLACE3000119  
C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224  
C-PLACE3000136

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C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084

C-PLACE3000148

5 C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//AB014572

C-PLACE3000160

C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742

C-PLACE3000194

C-PLACE3000199

10 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020

C-PLACE3000230

C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aay//92%//P53995

15 C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946

C-PLACE3000276

C-PLACE3000310

C-PLACE3000320

C-PLACE3000331

20 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640

C-PLACE3000352

C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739

25 C-PLACE3000362

C-PLACE3000365

C-PLACE3000388

C-PLACE3000413

C-PLACE3000425

30 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580

C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100

C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281

35 C-PLACE4000089

C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//AF091234

C-PLACE4000129

40 C-PLACE4000147

C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746

C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//AF000422

C-PLACE4000222

45 C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990

C-PLACE4000270

C-PLACE4000300

C-PLACE4000387

C-PLACE4000392

50 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200

C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217b.p//98%//AF000422

C-PLACE4000465

55 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267

C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

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C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800  
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655  
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709  
 5 C-THYRO1000070  
 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799  
 C-THYRO1000092  
 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039  
 10 C-THYRO1000124  
 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698  
 C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552  
 C-THYRO1000206  
 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//  
 15 P51523  
 C-THYRO1000253  
 C-THYRO1000270  
 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068  
 C-THYRO1000320  
 20 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563  
 C-THYRO1000368  
 C-THYRO1000381  
 C-THYRO1000387  
 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//  
 25 1325bp//99%//AF072864  
 C-THYRO10003957//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857  
 C-THYRO1000401  
 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663  
 C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 30 4.20E-98//408aa//42%//P19474  
 C-THYRO1000558  
 C-THYRO1000570  
 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//  
 AF140360  
 35 C-THYRO1000625  
 C-THYRO1000637  
 C-THYRO1000676  
 C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679  
 C-THYRO1000712  
 40 C-THYRO1000805  
 C-THYRO1000815  
 C-THYRO1000855  
 C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
 7.50E-57//315aa//43%//P32322  
 45 C-THYRO1000988  
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948  
 C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//  
 1479bp//66%//U38252  
 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and  
 50 TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276  
 C-THYRO1001262  
 C-THYRO1001271  
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-  
 ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701  
 55 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861  
 C-THYRO1001347  
 C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//  
 99%//AL080120

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C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%//AB014607  
 C-THYRO1001403  
 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427  
 C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//  
 5 AF078850  
 C-THYRO1001426  
 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580  
 C-THYRO1001480  
 10 C-THYRO1001487  
 C-THYRO1001584  
 C-THYRO1001661  
 C-THYRO1001746  
 C-THYRO1001772  
 15 C-THYRO1001854  
 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//  
 AF171060  
 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484  
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//  
 20 AF123534  
 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835  
 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692  
 C-Y79AA1000410  
 C-Y79AA1000539  
 25 C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//  
 AF091080  
 C-Y79AA1000802  
 C-Y79AA1000827  
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 30 C-Y79AA1000969  
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962  
 C-Y79AA1001061  
 C-Y79AA1001068  
 C-Y79AA1001216  
 35 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738  
 C-Y79AA1001511  
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 2.50E-14//410aa//24%//Q00547  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78//  
 40 227aa//40%//Q01820  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 45 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002210//YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//O16264  
 50 C-Y79AA1002220  
 C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 55 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

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C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//  
 51%/Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//  
 1444bp//98%/AF129534  
 5 C-HEMBA1000290  
 C-HEMBA1000459  
 C-HEMBA1000505  
 C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%/J04088  
 10 C-HEMBA1002503  
 C-HEMBA1002508  
 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%/AJ011972  
 C-HEMBA1003480  
 15 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%/P00736  
 C-HEMBA10036451//TTPD PROTEIN.//2.40E-10//289aa//23%/015736  
 C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%/AB023230  
 C-HEMBA1003667  
 20 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%/P23253  
 C-HEMBA1003827  
 C-HEMBA1003838  
 C-HEMBA1004055  
 25 C-HEMBA1004056  
 C-HEMBA1004086  
 C-HEMBA1004335  
 C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%/Q99471  
 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 30 TEIN).//3.10E-51//152aa//40%/Q61221  
 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%/AF201333  
 C-HEMBA1004507  
 C-HEMBA1004638  
 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%/P18583  
 35 C-HEMBA1004709  
 C-HEMBA1004860  
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%/AJ250308  
 C-HEMBA1005472  
 C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%/002193  
 40 C-HEMBA1005572  
 C-HEMBA1005780  
 C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%/AF082516  
 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%/Q61001  
 45 C-HEMBA1006124  
 C-HEMBA1006461  
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-  
 ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%/P25716  
 C-HEMBA1006617  
 50 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%/015509  
 C-HEMBA1006779  
 C-HEMBA1006796  
 C-HEMBA1006812  
 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%/U35832  
 55 C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%/AB028988  
 C-HEMBA1000240  
 C-HEMBA1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%/P22516



C-HEMBB1000335  
 C-HEMBB1000337  
 C-HEMBB1000554  
 C-HEMBB1000573  
 5 C-HEMBB1000749  
 C-HEMBB1000774  
 C-HEMBB1000835  
 C-HEMBB1001197  
 C-HEMBB1001315  
 10 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001500  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001619  
 15 C-HEMBB1001630  
 C-HEMBB1001665  
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031  
 C-HEMBB1001812  
 C-HEMBB1001834  
 20 C-HEMBB1001869  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//  
 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 25 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 30 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001925  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002152  
 35 C-HEMBB1002300  
 C-HEMBB1002381  
 C-HEMBB1002383  
 C-HEMBB1002534  
 C-MAMMA1000143  
 40 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//  
 P51523  
 C-MAMMA1000227  
 C-MAMMA1000257  
 C-MAMMA1000264  
 45 C-MAMMA1000270  
 C-MAMMA1000279  
 C-MAMMA1000372  
 C-MAMMA1000559  
 C-MAMMA1000752  
 50 C-MAMMA1000760  
 C-MAMMA1000778  
 C-MAMMA1000855  
 C-MAMMA1000859  
 C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN  
 55 H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033  
 C-MAMMA1000940  
 C-MAMMA1001073  
 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//

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AF067420  
 C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346  
 C-MAMMA1001202  
 C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978  
 5 C-MAMMA1001252  
 C-MAMMA1001296  
 C-MAMMA1001502  
 C-MAMMA1001630  
 C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910  
 10 C-MAMMA1001683  
 C-MAMMA1001715  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687  
 C-MAMMA1001760  
 15 C-MAMMA1001769  
 C-MAMMA1001785  
 C-MAMMA1001848  
 C-MAMMA1001874  
 C-MAMMA1001956  
 20 C-MAMMA1002009  
 C-MAMMA1002033  
 C-MAMMA1002155  
 C-MAMMA1002498  
 C-MAMMA1002545  
 25 C-MAMMA1002571  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640  
 C-MAMMA1002590  
 C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742  
 30 C-MAMMA1002618  
 C-MAMMA1002636  
 C-MAMMA1002646  
 C-MAMMA1002665  
 C-MAMMA1002708  
 35 C-MAMMA1002728  
 C-MAMMA1002744  
 C-MAMMA1002764  
 C-MAMMA1002765  
 C-MAMMA1002830  
 40 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178  
 C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590  
 C-MAMMA1002880  
 C-MAMMA1002892  
 45 C-MAMMA1002909  
 C-MAMMA1002941  
 C-MAMMA1002947  
 C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343  
 50 C-MAMMA1002973  
 C-MAMMA1002987  
 C-MAMMA1003003  
 C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542  
 C-MAMMA1003031  
 55 C-MAMMA1003089  
 C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843  
 C-NT2RM1000272

C-NT2RM1000341  
 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097  
 C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//  
 99%//AF103731  
 5 C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775  
 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//  
 27%//P49695  
 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458  
 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//  
 10 AF082516  
 C-NT2RM1001082  
 C-NT2RM1001112  
 C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//  
 AF053091  
 15 C-NT2RM2001360//Homo sapiens clone G40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798  
 C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//  
 2300bp//100%//AL110217  
 C-NT2RM2001803//Homo sapiens IkappaB kinase cbmplex associated protein (IKAP) mRNA, complete cds.//0//  
 2249bp//99%//AF044195  
 20 C-NT2RM4002504  
 C-NT2RP1000409  
 C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991  
 C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//  
 99%//AF173378  
 25 C-NT2RP1000796  
 C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//  
 P51522  
 C-NT2RP2001214  
 C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//  
 30 45%//Q05481  
 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334  
 C-NT2RP2002056  
 C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//  
 X65634  
 35 C-NT2RP2002333  
 C-NT2RP2002677  
 C-NT2RP2002755  
 C-NT2RP2002843  
 C-NT2RP2003101  
 40 C-NT2RP2003668  
 C-NT2RP2003799  
 C-NT2RP2004095  
 C-NT2RP2004300  
 C-NT2RP2004675  
 45 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
 CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//  
 22%//Q61687  
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//  
 AF045583  
 50 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444  
 C-NT2RP2005726  
 C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-  
 TRANSFERASE).//4.40E-55//358aa//42%//P51005  
 C-NT2RP2005980  
 55 C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%//AB020725  
 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK  
 ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131  
 C-NT2RP2006554

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C-NT2RP3000584  
 C-NT2RP3001115  
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//  
 1138bp//63%//AF193613  
 5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-)//1.30E-22//227aa//33%//P08458  
 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791  
 C-NT2RP3002402  
 C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215  
 C-NT2RP3002512  
 10 C-NT2RP3002713  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//  
 41%//P17564  
 C-NT2RP3002799  
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125  
 15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//  
 P51026  
 C-NT2RP3002955  
 C-NT2RP3002985  
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//  
 20 82%//U78090  
 C-NT2RP3003121  
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//  
 91%//AB011414  
 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//  
 25 AF071592  
 C-NT2RP3003155  
 C-NT2RP3003157  
 C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455  
 C-NT2RP3003264  
 30 C-NT2RP3003346  
 C-NT2RP3003403  
 C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//  
 743bp//90%//AF071317  
 C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009  
 35 C-NT2RP3003572  
 C-NT2RP3003576  
 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885  
 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//2.20E-13//146aa//42%//P14209  
 40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//  
 2047bp//95%//AL080155  
 C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294  
 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//  
 45 924bp//89%//AF130457  
 C-NT2RP3003828  
 C-NT2RP3003932  
 C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//2739bp//  
 99%//AL050019  
 C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692  
 50 C-NT2RP3004028  
 C-NT2RP3004041  
 C-NT2RP3004051  
 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091  
 C-NT2RP3004093  
 55 C-NT2RP3004095  
 C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-  
 229//1560bp//78%//AF126747  
 C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

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DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640  
 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948  
 C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1J//1.30E-14//242aa//24%//Q00808  
 C-NT2RP3004332  
 5 C-NT2RP3004349  
 C-NT2RP3004470  
 C-NT2RP4000035  
 C-NT2RP4000049  
 C-NT2RP4000102  
 10 C-NT2RP4000167  
 C-NT2RP4000515  
 C-NT2RP4000517  
 C-NT2RP4000519  
 C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117  
 15 C-OVARC1000092  
 C-OVARC1000533  
 C-OVARC1000678  
 C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//  
 0//2032bp//99%//AL133014  
 20 C-OVARC1000802  
 C-OVARC1000890  
 C-OVARC1000891  
 C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//  
 82%//AB005549  
 25 C-OVARC1001072  
 C-OVARC1001117  
 C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192  
 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//  
 X62083  
 30 C-OVARC1001329  
 C-OVARC1001341  
 C-OVARC1001376  
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
 AF016507  
 35 C-OVARC1001873  
 C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//1.60E-81//212aa//70%//P34547  
 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-  
 40 241//1124bp//98%//AF135421  
 C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234  
 C-PLACE1001076  
 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742  
 C-PLACE1001366  
 45 C-PLACE1001545  
 C-PLACE1001608  
 C-PLACE1002004  
 C-PLACE1002256  
 C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233  
 50 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146  
 C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//  
 AF079765  
 C-PLACE1003383  
 C-PLACE1003864  
 55 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267  
 C-PLACE1004913  
 C-PLACE1004979  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

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C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148  
 C-PLACE1005128  
 C-PLACE1005162  
 5 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//  
 96%//AF113539  
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//  
 7.60E-97//1287bp//67%//AJ010046  
 10 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//  
 6.80E-09//267aa//30%//P29128  
 C-PLACE1005611//Mus musculus mRNA for mDjIO, complete cds.//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005802  
 C-PLACE1005850  
 C-PLACE1005898  
 15 C-PLACE1005932  
 C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542  
 C-PLACE1006360  
 C-PLACE1006795  
 20 C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
 NUCLEASE).//1.90E-08//122aa//36%//P16658  
 C-PLACE1007557  
 C-PLACE1007807  
 C-PLACE1008181  
 25 C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114  
 C-PLACE1008455  
 C-PLACE1008941  
 C-PLACE1009935  
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804  
 C-PLACE1011891  
 30 C-PLACE10118967//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969  
 C-PLACE2000003  
 C-PLACE2000132  
 C-PLACE2000170  
 C-PLACE2000335  
 35 C-PLACE3000124  
 C-PLACE3000158  
 C-PLACE3000207  
 C-PLACE3000221  
 C-PLACE3000271  
 40 C-PLACE3000304  
 C-PLACE3000322  
 C-PLACE3000341  
 C-PLACE3000373  
 C-PLACE3000399  
 45 C-PLACE3000401  
 C-PLACE3000402  
 C-PLACE3000406  
 C-PLACE3000475  
 50 C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640  
 C-PLACE4000093  
 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//  
 AF146689  
 55 C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//  
 1612bp//97%//AL117455  
 C-PLACE4000247  
 C-PLACE4000250  
 C-PLACE4000252

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C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200  
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201  
 C-PLACE4000320  
 C-PLACE4000344  
 5 C-PLACE4000367  
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//7.20E-22//54aa//62%//Q01576  
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//  
 0//2159bp//98%//AL117654  
 10 C-PLACE4000487  
 C-PLACE4000494  
 C-PLACE4000521  
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164  
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mito-  
 15 chondrial protein, complete cds.//0//2384bp//99%//AF047690  
 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//  
 AB021663  
 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333  
 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//  
 20 AF118566  
 C-THYRO1001142  
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//  
 62%//005481  
 C-THYRO1001320  
 25 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//  
 0//1010bp//98%//AL050159  
 C-THYRO1001602  
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652  
 C-THYRO1001828  
 30 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//  
 AF157833  
 C-Y79AA1001167  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//  
 4708bp//99%//AF055084  
 35 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 C-HEMBA1006092  
 C-HEMBA1006406  
 C-HEMBB1000790  
 40 C-HEMBB1000917  
 C-HEMBB1002280  
 C-MAMMA1000802  
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//  
 P20931  
 45 C-MAMMA1002597  
 C-MAMMA1002868  
 C-NT2RP2003161  
 C-NT2RP2003339  
 C-NT2RP3001282  
 50 C-PLACE1001761  
 C-PLACE1004491  
 C-PLACE1004686  
 C-PLACE1005574  
 C-PLACE1006382  
 55 C-PLACE1006792  
 C-PLACE3000455  
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430  
 C-THYRO1000916

C-HEMBA1000327  
 C-HEMBA1000637  
 C-HEMBA1001967  
 C-MAMMA1000266  
 5 C-NT2RP2002979  
 C-PLACE1007866  
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)  
 (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%//Q13177  
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%//P52740  
 10 C-THYRO1001637  
 C-MAMMA1002215  
 C-MAMMA1002721  
 C-NT2RP2002070

15 Homology search result 14.

**[0334]** Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%//061712  
 25 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 (LEURS).//6.40E-99//457aa//45%//Q09996  
 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%//X02344  
 C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.//0//1759bp//99%//  
 AF124490  
 30 C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME- I.//3.80E-25//166aa//36%//  
 Q09884  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//  
 AF196304  
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%//  
 AF085356  
 35 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 1.90E-12//368aa//24%//P08553  
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%//P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%//P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31 %//P48555  
 40 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738  
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//1.00E-86//146aa//56%//Q61221  
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%//  
 AF030131  
 45 C-HEMBA1000304//Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-  
 131//712bp//91%//U16802  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-  
 49//107aa//91%//035594  
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//  
 50 AF174601  
 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%//AB026491  
 C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%//Q02357  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa//31%//P22279  
 55 C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa//38%//P18490  
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa//36%//Q01755  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS).//2.60E-12//73aa//41%//P02826



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- C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340
- C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529
- 5 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25 %//Q05481
- C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aap//32%//Q60865
- C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573
- 10 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
- C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856
- C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//Q43295
- C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776
- 15 C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868
- C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689
- C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366
- 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124
- C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
- C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.40E-12//131aa//38%//Q01485
- 25 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088
- C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461
- C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043
- 30 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059
- C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730
- 35 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646
- C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221
- C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
- C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
- 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686
- C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358
- C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081
- 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091
- C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221
- C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599
- 50 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
- C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850
- 55 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166
- C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%//P19065
- C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

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C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141  
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//  
 P42803  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%//  
 5 Q63679  
 C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCES-  
 SORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//  
 365aa//33%//P33450  
 10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
 plete cds.//0//1707bp//98%//AF072247  
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//  
 P54787  
 C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//  
 15 100%//AB029042  
 C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%//  
 AF195883  
 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).//  
 1.10E-38//87aa//96%//P55288  
 20 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009  
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, com-  
 plete cds.//7.60E-59//998bp//64%//AF098066  
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//  
 1637bp//99%//AF125158  
 25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676  
 C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479  
 C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//  
 AF159025  
 30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%//Q07230  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//5.70E-51//234aa//41%//Q09332  
 C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//  
 35 9.30E-36//395aa//26%//Q63342  
 C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535  
 C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//  
 1850bp//99%//AF000145  
 C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114  
 40 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete  
 cds.//0//2149bp//99%//AB032252  
 C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-  
 271//1583bp//88%//U92703  
 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357  
 45 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//  
 P79293  
 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//  
 50 P43694  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.00E-17//267aa//29%//  
 P18161  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226  
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 55 NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087  
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537  
 C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//96%//Q62415  
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

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- 1847bp//99%//AF092563  
C-HEMBA1002417//mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)//1.00E-121//489aa//52%//P39447  
C-HEMBA1002419//TRICHOHYALIN//1.90E-09//299aa//24%//P22793  
5 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74//4.20E-24//109aa//55%//Q00994  
C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT)//3.50E-50//199aa//61%//P98175  
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.10E-12//285aa//31%//P17437  
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1//6.80E-53//257aa//36%//P48732  
10 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//0//2432bp//99%//AJ011972  
C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//0//1605bp//97%//AF016903  
C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds//5.30E-51//768bp//68%//AF055993  
15 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//6.80E-305//951bp//99%//AF075587  
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7)//5.00E-37//268aa//34%//P06746  
C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds//7.80E-237//1522bp//85%//AB011126  
20 C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds//2.90E-176//1024bp//88%//D87671  
C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds//3.40E-54//319bp//76%//AF153879  
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//8.2E-314//1437bp//99%//AF071185  
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4//2.00E-304//1383bp//99%//AJ132819  
25 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n//1.50E-44//188aa//52%//Q09297  
C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.30E-15//371aa//25%//Q05481  
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//2.00E-34//300aa//34%//P16157  
30 C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//4.40E-06//324aa//24%//P32380  
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//1.20E-27//63aa//100%//P14646  
35 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//3.80E-25//534aa//24%//Q02224  
C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds//1.40E-171//1552bp//75%//U20286  
C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA//0//1558bp//99%//AF054182  
40 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS)//1.30E-09//121aa//40%//P35858  
C-HEMBA1003077//SLIT PROTEIN PRECURSOR//2.60E-15//199aa//31%//P24014  
C-HEMBA1003096//Mouse 19.5 mRNA, complete cds//5.60E-117//1139bp//72%//M32486  
C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds//6.20E-273//1253bp//99%//AF155096  
45 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)//8.50E-51//221aa//33%//P41940  
C-HEMBA1003148//Homo sapiens mRNA for dachshund protein//0//1583bp//99%//AJ005670  
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61)//5.90E-74//134aa//53%//P44551  
50 C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds//8.50E-87//285bp//90%//AF129534  
C-HEMBA1003235//TROPOMYOSIN//2.30E-06//109aa//33%//Q02088  
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-)//7.20E-41//245aa//42%//Q06548  
55 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR//6.00E-11//239aa//32%//P32506  
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds//5.40E-229//1043bp//99%//AB024436  
C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10)//7.20E-28//126aa//51%//

Q38997

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%//Q02224  
 C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//  
 7.80E-13//297aa//30%//P18616  
 5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-  
 255//1179bp//99%//AF095192  
 C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%//P37709  
 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139  
 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//  
 10 58%//P00736  
 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%//P50480  
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%//P53384  
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-  
 MA-I).//1.20E-31//71aa//100%//P16874  
 15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 7.90E-49//279aa//32%//P19474  
 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%//Q13330  
 C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%//P26039  
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10//  
 20 118aa//35%//P19682  
 C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%//AB026125  
 C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//  
 97%//AB015344  
 C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%//O15736  
 25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%//Q13207  
 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-  
 09//611aa//22%//P23253  
 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//  
 423aa//47%//P34629  
 30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%//Q13105  
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%//P53973  
 C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//  
 1.70E-44//501bp//67%//AF037339  
 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
 35 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665  
 C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-  
 81//511bp//86%//U17343  
 C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//  
 1204bp//84%//AF084259  
 40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp//  
 95%//AF090402  
 C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484  
 C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//1.20E-105//1192bp//70%//AF030430  
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//  
 45 89aa//46%//P16372  
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%//  
 AF091234  
 C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%//Q14141  
 C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%//AF067855  
 50 C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%//  
 P34529  
 C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%//P51153  
 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%//P40991  
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748  
 55 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.70E-217//1217bp//88%//  
 AF095927  
 C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN  
 CL-6).//2.00E-43//98aa//84%//Q08755

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C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds.//1.10E-152//1403bp//69%//AF043725

C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.80E-257//738bp//99%//AF092094

5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp//99%//AF022795

C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103

C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676

C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471

10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516

C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494

C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1437bp//99%//AF125158

C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-CLOPHILIN-10).//3.20E-32//148aa//52%//P52017

15 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221

C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333

C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107

20 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841

C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291

25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844

C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583

C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749

C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743

30 C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405

C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082

C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%//L39060

35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547

C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851

C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%//Q00004

C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aapb//26%//U72515

40 C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%//P25386

C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401

C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036

45 C-HEMBA1004973//ZINC-BINDING PROTEIN A337/4.10E-08//121aa//33%//Q02084

C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474

C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947

C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290

C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//AF080561

50 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941

C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004

C-HEMBA1005206//Drosophila simulans anon73Bl gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308

55 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%//P39929

C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581

C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743

C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

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AF071787

C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//3.90E-126//1097bp//75%//AF200357

5 C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//2.00E-213//537bp//99%//AF041248

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//O02193

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%//Q60809

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340

10 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157

C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929

C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%//D86949

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270

15 C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN).//0.00000009//213aa//27%//P09492

C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.30E-54//562aa//29%//P34036

C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds.//8.00E-211//962bp//99%//AF072933

C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%//AJ249128

20 C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81 %//Q15768

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.40E-17//167aa//34%//P25296

25 C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789

C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%//P51522

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516

30 C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%//AB019435

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001

C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%//AF098066

C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25 %//Q93794

35 C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//155 lbp//99%//AF048693

C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.90E-19//215aa//39%//P05142

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23//151aa//37%//P16372

40 C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//62aa//53%//P42698

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265

45 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.00E-210//490aa//77%//P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//30%//P32505

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.20E-12//215aa//23%//P70473

50 C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%//AF005050

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043

55 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//O02193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160

C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds.//2.00E-277//1729bp//85%//U93563

C-HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.//1.40E-270//1224bp//

100%//U96750  
 C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%//Q01552  
 C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//  
 97%//P55786  
 5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%//O60879  
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-  
 ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716  
 C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//2.80E-206//1107bp//83%//U06944  
 C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%//  
 10 AF190774  
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//  
 38%//Q58323  
 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//O15509  
 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
 15 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
 INTERGENIC REGION.//3.30E-22//241aa//31%//P53196  
 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 0.00000043//111aa//40%//Q01485  
 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//  
 20 91%//AF152492  
 C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644  
 C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN.//2.00E-59//378aa//39%//P16258  
 C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%//  
 AB018566  
 25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//  
 U35832  
 C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271//  
 1234bp//99%//AF118649  
 C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%//  
 30 AF004828  
 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/4)GlcNAc alpha-2,3-sialyltransferase.//1.90E-80//  
 447bp//89%//X74570  
 C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN  
 A) (DLC-A).//2.40E-188//391aa//89%//Q90828  
 35 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF  
 100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568  
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//  
 92%//AF125042  
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929  
 40 C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085  
 C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//  
 1588bp//99%//AF139658  
 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//  
 AF196304  
 45 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060  
 C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.//5.00E-58//330bp//95%//  
 AF176707  
 C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice var-  
 iant 1, complete cds.//0//1519bp//99%//AF127479  
 50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941  
 C-HEMBA1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%//AF151809  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187//  
 1582bp//80%//AF084928  
 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 55 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799  
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521  
 C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLA-  
 SE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

- C-HEM BB1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385
- C-HEM BB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEDB.5//2.70E-12//112aa//47%//Q09530
- 5 C-HEM BB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516
- C-HEM BB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256
- C-HEM BB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
- 10 C-HEM BB1000593//Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864
- C-HEM BB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970
- C-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671
- 15 C-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723
- C-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475
- C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
- C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105
- 20 C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956
- C-HEM BB1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008
- 25 C-HEM BB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122
- C-HEM BB1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598
- C-HEM BB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910
- 30 C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974
- C-HEM BB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575
- C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523
- 35 C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087
- C-HEM BB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.60E-52//331bp//80%//AF010144
- C-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803
- 40 C-HEM BB1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032
- C-HEM BB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435
- C-HEM BB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267
- 45 C-HEM BB1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357
- C-HEM BB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938
- C-HEM BB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897
- C-HEM BB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157
- 50 C-HEM BB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719
- C-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081
- C-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703
- 55 C-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//2.10E-65//458bp//79%//D63850
- C-HEM BB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175
- C-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441



C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-AT-  
 PASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342  
 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167  
 15 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLG42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 P18720  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//  
 20 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 25 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)  
 30 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN  
 35 KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//  
 40 1045bp//99%//AF118649  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544  
 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749  
 C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-  
 136//660bp//98%//AF105421  
 C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//  
 50 Z47553  
 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226  
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 55 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//  
 2.60E-164//1044bp//87%//AF197060  
 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

P51523

C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.20E-109//864bp//76%//X99836

C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%//AB015132

5 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%//Q09232

C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883

C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%//P48365

10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.).//4.40E-33//250aa//33%//P42660

C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%//AF172451

C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524

15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%//O14646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9.00E-299//1033aa//55%//P87115

20 C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%//P53500

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711

25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%//AF117892

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674

30 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746

C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946

C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%//AF151830

35 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//AF067420

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338

40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978

C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%//AF184275

45 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa//30%//P34537

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

50 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//P20931

C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.50E-129//260aa//92%//P52623

55 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.50E-276//1561bp//90%//M61764

C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989

C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687  
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
 5 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa//36%//P21573  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//1987bp//99%//AF112204  
 10 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%//Q58556  
 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 15 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230  
 C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664  
 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880  
 20 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667  
 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.80E-217//310aa//86%//PP70541  
 25 C-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.00E-190//1624bp//76%//AF068748  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//AJ011679  
 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//AF190795  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 35 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623  
 C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//AF098462  
 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//337aa//31%//P43571  
 C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0//1910bp//99%//AF065214  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640  
 45 C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742  
 C-MAMMA1002619//PROBABLE UBIQUITTIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITTIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.50E-16//159aa//37%//Q09931  
 50 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.10E-45//618aa//26%//P27550  
 55 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3E-317//1942bp//85%//AF018261  
 C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

- 2.20E-25//330bp//77%//AF011794  
 C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%//U58883  
 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178  
 C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590  
 C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//85%//P48059  
 C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//35%//P48060  
 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
 C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343  
 C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874  
 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746  
 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851  
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//1533bp//99%//AF077952  
 C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584  
 C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//1178bp//86%//AF071316  
 C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735  
 C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062  
 C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//5.00E-13//592aa//24%//P47179  
 C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//592bp//97%//AF123052  
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110  
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596  
 C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671  
 C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190  
 C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//32%//P34537  
 C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843  
 C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072  
 C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959  
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902  
 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072  
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aa//47%//O42643  
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AJ245820  
 C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//U81002  
 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882  
 C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//3012bp//99%//AB016789  
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028  
 C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds.//0//2766bp//99%//AF055995  
 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

- C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423
- C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.7/0//1599bp//99%//AF152462
- 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//1016bp//94%//AF179212
- C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915
- C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185//1486bp//81%//AF084928
- C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700
- C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
- C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
- 15 C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
- C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
- C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%//AF038957
- C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989
- C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
- 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
- C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227//1043bp//99%//AF141310
- 30 C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202
- C-NT2RM1000772//VEGETATABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808
- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%//Z97207
- C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- 35 C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8
- C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157
- C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0//2206bp//99%//AF077033
- 40 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.40E-244//1113bp//99%//AF043733
- C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%//AF126799
- 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
- C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537
- C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
- 50 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583
- C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa//26%//P46577
- C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2230bp//99%//AF030233
- 55 C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.60E-13//119aa//36%//Q09701
- C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

Q99383

C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%/P08487

5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%/Q05481

C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%/U88964

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%/P54197

10 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%/P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%/P54703

15 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.30E-36//160aa//40%/P50102

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%/AF067223

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%/P14918

20 C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%/O48660

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%/P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%/U48251

25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.70E-68//419aa//36%/P50849

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.60E-54//344aa//33 %//P32802

30 C-NT2RM2000407//Mus musculus semaphorin 6A mRNA, complete cds.//9.70E-201//826bp//84%/AF030430

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%/Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%/P36113

35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%/P22211

C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%/P41823

C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%/U78304

C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%/AF061243

40 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%/P17437

C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%/AF032108

C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-187//741aa//46%/P73505

45 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%/P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%/AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%/AF179221

50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%/AJ245620

C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%/U35776

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%/Q08170

55 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.70E-142//285aa//90%/P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa//36%/Q15404

C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%/AF121141

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C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%/P28160  
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.70E-53//266aa//43%/P41877  
5 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa//98%/P23514  
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%/AB015046  
C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%/Q60809  
10 C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%/AF100757  
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//26%/P46577  
C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%/AF053091  
15 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%/P05143  
C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%/P48724  
C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//177aa//32%/P97924  
20 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.30E-180//328aa//99%/P13264  
C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%/P53995  
C-NT2RM2001324//ZYGXIN.//6.80E-55//200aa//41%/Q04584  
25 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%/Q00808  
C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%/AJ007509  
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121//437aa//57%/P52569  
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//90aa//42%/P38660  
30 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.30E-61//312aa//44%/P19474  
C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%/AF032667  
C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%/AJ132440  
35 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%/AF084458  
C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%/P35844  
C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.20E-142//566aa//56%/P52591  
C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%/AF084458  
40 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%/AF111162  
C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%/P20107  
C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0//2471bp//99%/AF044195  
45 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds.//6.20E-16//464bp//62%/AFQ83391  
C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%/Q07230  
C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0//1843bp//94%/U21155  
50 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//30%/Q09674  
C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253//1170bp//99%/AB028600  
C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//5.70E-130//536aa//49%/P50544  
55 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//0//1774bp//98%/AB032251  
C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

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ZYME).//7.20E-16//381aa//27%//Q09931  
 C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792  
 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609  
 5 C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458  
 C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742  
 C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422  
 C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799  
 10 C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195  
 C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa//39%//P32657  
 C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759  
 15 C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010  
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692  
 C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818  
 C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182  
 20 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320  
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250  
 25 C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816  
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838  
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730  
 30 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L//3.10E-12//206aa//30%//Q09782  
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796  
 35 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837  
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789  
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878  
 40 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990  
 C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//AF053091  
 45 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840  
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435  
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%//P49695  
 50 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805  
 C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928  
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167  
 55 C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146  
 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101



- C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//1.20E-157//321aa//61%/P26639
- C-NT2RM4000156//H.sapiens HPBR11-7 gene.//3.60E-21//785bp//60%/X67336
- C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//1946bp//99%/AJ271784
- 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//686aa//23%/P25386
- C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%/P16381
- C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%/Q16600
- C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%/P10962
- 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%/L20303
- C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%/AF030430
- C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%/M99438
- 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637
- C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%/Q24371
- C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%/P35292
- C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%/AF195418
- 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769
- C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271//2085bp//77%/AF062476
- C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%/Q10297
- 25 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%/AF097025
- C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%/P04280
- C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//29%/P39955
- C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.10E-11//394aa//24%/P16884
- 30 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%/Q07230
- C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%/Q04652
- C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%/P26337
- 35 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%/Q00808
- C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%/P27550
- C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%/P51178
- 40 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747/1.20E-28//180aa//30%/P74168
- C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136//1104bp//77%/AF022789
- C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%/P52154
- 45 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%/AF221712
- C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.//0//2184bp//99%/D88208
- C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%/Q99676
- C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%/AF084521
- 50 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%/P40682
- C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%/P02750
- C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%/Q05481
- 55 C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%/Q06138
- C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%/AF077032
- C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%/Q09820

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C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%/P38682  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//5.90E-86//292aa//48%/Q09417  
 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D//1.00E-11//103aa//38%/Q01704  
 5 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//4.10E-197//445aa//78%/Q27969  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1//1.10E-48//218aa//43%/Q03532  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135//9.50E-135//375aa//60%/P52742  
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//0//2310bp//99%/AF004828  
 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds//3.10E-148//1445bp//72%/U65079  
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds//4.30E-55//289bp//77%/AF129131  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)//3.50E-35//124aa//65%/P54676  
 15 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD)//2.30E-31//334aa//30%/P08503  
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds//1.80E-39//728bp//64%/D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)//1.00E-28//171aa//37%/P32626  
 20 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION//8.10E-30//265aa//33%/P53742  
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds//0//2300bp//99%/AF155103  
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds//0//2524bp//99%/AB019494  
 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//2.20E-237//1079bp//99%/AF098799  
 25 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds//0//1962bp//87%/AF020526  
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds//0//1918bp//99%/AF047711  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.40E-118//444aa//46%/P73505  
 30 C-NT2RM4001483//ZINC FINGER PROTEIN 136//5.10E-106//357aa//55%/P52737  
 C-NT2RM4001566//NECDIN//9.80E-44//227aa//41%/P25233  
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds//1.50E-284//1082bp//90%/AF071317  
 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION//7.60E-56//213aa//49%/P31380  
 C-NT2RM4001597//M.musculus red-1 gene//12.10E-171//1414bp//78%/X92750  
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)/J/2.60E-32//203aa//39%/Q12600  
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)//1.50E-93//278aa//38%/Q13368  
 40 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION//2.70E-84//410aa//42%/P37339  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT)//8.90E-141//354aa//72%/Q14141  
 C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds//0//1922bp//100%/AF179221  
 45 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.)/J/4.10E-186//639aa//58%/Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1)//7.90E-66//311aa//35%/Q03164  
 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1)//5.10E-07//263aa//30%/P16112  
 50 C-NT2RM4001813//LECTIN BRA-2//0.00000048//114aa//30%/P17346  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds//8.10E-300//1395bp//98%/M37712  
 55 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)/7/2.90E-55//325aa//37%/P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//5.90E-161//481aa//56%/P51523  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT)//6.50E-22//126aa//46%/P79779

- C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%//Y17711
- C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%//Q15404
- 5 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486
- C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851
- C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162
- C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330
- 10 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%//P51523
- C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170
- C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935
- 15 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260
- C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419
- C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%//U82267
- 20 C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71 %//AF117755
- C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//AF072758
- 25 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652
- C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%//AF176085
- C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784
- C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014
- 30 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940
- C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535
- C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590
- C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640
- 35 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430
- C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%//Q07803
- C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%//AF157028
- 40 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809
- C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808
- C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778
- 45 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%//P27095
- C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%//AF129131
- C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515
- 50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808
- C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137
- C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%//AF055899
- 55 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962
- C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019
- C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

- C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).//  
2.30E-101//488aa//45%//O32038
- C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385
- C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449
- 5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//  
AF193608
- C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834
- C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471
- C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859
- 10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//  
951bp//98%//AF011792
- C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357
- C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//  
1155bp//87%//AB015895
- 15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
plete cds.//1.30E-275//1249bp//99%//AF053551
- C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447
- C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343
- C-NT2RP1000363//R.norvegicus LL5 mRNA//7.90E-262//1175bp//83%//X74226
- 20 C-NT2RP1000376//Homo sapiens Ca<sup>2+</sup>-independent phospholipase A2 long isoform (iPLA2) mRNA, complete  
cds.//0//2252bp//96%//AF102989
- C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%//  
P55161
- C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-  
94//1019bp//63%//AF111423
- 25 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-  
CRYSTALLIN).//2.40E-10//227aa//25%//Q08257
- C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624
- C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//  
30 254aa//47%//P34580
- C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653
- C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%//  
AF039688
- C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM  
35 GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194
- C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101
- C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//8.20E-83//345aa//47%//Q61068
- 40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-  
27//193aa//35%//P49020
- C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%//  
P97367
- C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233
- 45 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721
- C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
1687bp//99%//AF145020
- C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379
- 50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
cds.//0//2186bp//99%//AF101434
- C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//  
99%//AF173378
- C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
55 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566
- C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN  
ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960
- C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase AI (PDE9A) mRNA, complete cds.//0//1494bp//99%//

AF067223

C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%//L01790

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291

C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//284aa//25%//P40074

C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917

C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//100%//AJ005257

C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//O35566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//271aa//89%//P47758

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

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C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//79aa//55%//O34136

C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-17//726aa//47%//P51523

5 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//7.1.80E-22//184aa//34%//Q01730

C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749

10 C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//2245bp//99%//AF155109

C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON).//9.40E-16//45aa//100%//P49446

C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418

15 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51//383aa//32%//P33450

C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//AJ242730

C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356

20 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//P41877

C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//AF175966

C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585

25 C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891

C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329

C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632

30 C-NT2RP2000183//DIHYDROXYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675

C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//99%//AF153605

C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568

35 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558

C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556

C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//7.10E-12//213aa//23%//P35251

40 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//1043bp//99%//U78723

C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.60E-27//576aa//25%//Q10297

C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676

45 C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//1193bp//99%//U82381

C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760

C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//99%//U83981

50 C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010

C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910

C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265

55 C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844

C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238

C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

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C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.30E-27//349aa//32%//Q01577

C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%//O32038

5 C-NT2RP2000764//NIFS PROTEIN//6.60E-36//252aa//42%//P12623

C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195

C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A)//5-.60E-08//179aa//29%//Q99104

10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120)//1.10E-07//96aa//29%//P13466

C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT//7.90E-08//172aa//28%//P26174

C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811

15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2//0//694aa//99%//O60841

C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135

C-NT2RP2000931//MATRIN 3//2.40E-289//467aa//95%//P43244

C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds.//0//2767bp//99%//AF130464

C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704

20 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE)//5.80E-46//222aa//45%//Q20939

C-NT2RP2001081//SYNAPTOTAGMIN IV//4.20E-118//430aa//54%//P50232

C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440

C-NT2RP2001168//VERPROLIN//1.50E-09//143aa//33%//P37370

25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT)//6.00E-10//88aa//38%//P18722

C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//2.00E-128//409aa//45%//Q05481

C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC)//2.20E-10//366aa//28%//P14105

30 C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT)//4.40E-91//179aa//99%//P28663

C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN//8.30E-39//161aa//34%//P20107

C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)//5.50E-116//311aa//71%//Q13829

35 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//2.00E-11//403aa//25%//Q02817

C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//8.40E-192//581aa//54%//P93647

C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004

40 C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds.//1.9e-316//1428bp//100%//AB020981

C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//9.00E-112//742bp//82%//U76759

C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334

C-NT2RP2001460//TRICHOHYAUN//1.00E-14//521aa//24%//P37709

45 C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//3.20E-297//2206bp//75%//AF093097

C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//0//2502bp//99%//Y14494

C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2326bp//99%//AF035586

C-NT2RP2001560//NAV2 PROTEIN//0.00000015//219aa//27%//Q60992

50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I//8.20E-29//294aa//31%//Q09837

C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE//0.000000036//127aa//36%//P30957

C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1748bp//99%//AF196304

55 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//6.10E-12//184aa//31%//P24391

C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067

C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

NA, complete cds.//0//1287bp//99%//AF058718  
 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897  
 5 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068  
 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANS-FERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//797%//P14324  
 10 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523  
 C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009  
 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754  
 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008  
 15 C-NT2RP2001883//Homo sapiens CGI-01 - protein mRNA, complete cds.//0//2306bp//99%//AF132936  
 C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161  
 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946  
 20 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177//1538bp//74%//AF062378  
 C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%//AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%//Q08469  
 25 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%//P35331  
 C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0//1664bp//99%//AJ130894  
 C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0//2510bp//99%//AF083217  
 30 C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306  
 C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490  
 C-NT2RP2002079//HISTONE HI, GONADAL.//4.40E-11//214aa//34%//P02256  
 35 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//33 89bp//99%//AJ007509  
 C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634  
 C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-TOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107  
 40 C-NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.//0//2809bp//99%//AB021868  
 C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0//3118bp//91%//L38621  
 45 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418  
 C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568  
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521  
 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp//99%//AB015594  
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240//1105bp//99%//AF038958  
 50 C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp//93%//AJ242972  
 C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620  
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289  
 55 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%//Q02386  
 C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.//3.70E-34//668bp//61%//AF105427



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C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa//26%//Q11073  
C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523  
5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%//P12815  
C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%//P55345  
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa//30%//O14345  
C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%//P55194  
15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%//P29764  
C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922  
20 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%//AF038392  
C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%//Q18964  
C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%//P52737  
25 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%//P51669  
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%//P10129  
C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190  
30 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%//Q13829  
C-NT2RP2003121//Mus musculus enhancer of polycbmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%//AF079765  
35 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%//Q04652  
C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117  
C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%//Q08170  
40 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%//D67025  
C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%//AF006264  
C-NT2RP2003228//H.sapiens PI-Cdc21 mRNA.//0//2870bp//98%//X74794  
45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657  
C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811  
50 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069  
C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%//P30771  
C-NT2RP2003286//PROBABLE RNA 3'- TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%//Q23400  
55 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572  
C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%//Q07866  
C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%//P17886

- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.60E-14//332aa//32%//P26337
- C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754
- 5 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
- C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386
- C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//Q61068
- 10 C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5.00E-131//269aa//91%//P38378
- C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2194bp//99%//AF126799
- 15 C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//3012bp//99%//AF125158
- C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.40E-14//106aa//46%//P04175
- C-NT2RP2003513//Homo sapiens mRNA for paralemmin.//0//2137bp//97%//Y14770
- 20 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783
- C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158
- C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.70E-17//148aa//34%//P74261
- 25 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//2.10E-59//270aa//46%//P19474
- C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds.//4.80E-82//530bp//85%//AF130367
- 30 C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2442bp//99%//AF030233
- C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215
- C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786
- 35 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637
- C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.//0//2018bp//99%//AF073344
- 40 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.40E-29//85aa//72%//Q05481
- C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.70E-75//147aa//93%//P51669
- C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620
- 45 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201
- C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.70E-21//137aa//43%//Q11076
- 50 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955
- C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.//0//2807bp//99%//AF205601
- C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954
- 55 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.50E-23//200aa//30%//O09175
- C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//1.40E-16//664aa//720%//

P39702

C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//  
2.30E-53//141aa//78%/P20290

C-NT2RP2004041//SYNAPSINS IA AND B//0.00000074//159aa//32%/P17599

5 C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288//  
1994bp//81%/AF156529

C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
SE)//5.40E-30//319aa//31%/Q01513

C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%/Y12781

10 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49)//  
5.60E-31//424aa//28%/Q07231

C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%/AF003998

15 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%/AB015982

C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%/AB015718

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
9.90E-12//427aa//26%/P19246

20 C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//6.40E-117//  
1122bp//72%/AF200357

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR//1.40E-16//334aa//24%/P32857

C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13//1.30E-51//505aa//  
29%/Q07878

25 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR//9.30E-15//  
126aa//39%/P38120

C-NT2RP2004392//MNN4 PROTEIN//1.40E-11//143aa//27%/P36044

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//  
99%/AB028069

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%/AF155739

30 C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%/AF180920

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%/AF090190

C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%/Q09903

35 C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//  
7.30E-07//352aa//23%/P07197

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%/AJ006291

C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
2.60E-07//426aa//23%/P19246

40 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I//5.60E-64//616aa//  
33%/Q92355

C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%/U40750

45 C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//  
7.30E-07//352aa//23%/P07197

C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1)//1.30E-  
26//190aa//41%/P38692

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA  
LIGASE) (LEURS)//9.50E-73//153aa//59%/Q10490

50 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//3.70E-135//414aa//62%/P53588

C-NT2RP2004816//H58 PROTEIN//9.00E-173//327aa//98%/P40336

C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN)//4.20E-09//804aa//  
22%/Q61687

55 C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%/AB007144

C-NT2RP2004959//P54 PROTEIN PRECURSOR//0.00000095//297aa//20%/P13692

C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-

- 228//1666bp//75%//U56732  
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386  
 C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//  
 1.80E-99//376aa//43%//P19474
- 5 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779  
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447  
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)  
 (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4.00E-91//218aa//44%//  
 Q92089
- 10 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3  
 ALPHA).//2.00E-173//273aa//57%//P34466  
 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//  
 X98743
- 15 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE  
 L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921  
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%//  
 AF045583
- C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050  
 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509
- 20 C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0//  
 1262bp//99%//AF090385  
 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025  
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053  
 C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%//  
 AF060219
- 25 C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//  
 780bp//100%//AF036144  
 C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//  
 99%//AF124735
- 30 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709  
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//  
 38%//P32660  
 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
 plete cds.//0//2199bp//99%//AF072247
- 35 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SEN1) mRNA, complete cds.//1.30E-52//  
 753bp//67%//AF149770  
 C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823  
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059  
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//1.20E-13//185aa//38%//Q08170
- 40 C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%//  
 AF113540  
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete  
 cds.//1.20E-13 0//608bp//99%//AF070652
- 45 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127  
 C-NT2RP2005476//Human pI90-B (pI90-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032  
 C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.//1.80E-175//1102bp//83%//  
 AF053628
- C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418
- 50 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742  
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PRO-  
 TEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.20E-81//166aa//88%//P36876  
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803  
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//  
 3994bp//99%//AF092563
- 55 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.40E-304//1687bp//85%//AF035526  
 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171  
 C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

- C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2.00E-20//181aa//36%//Q39366
- 5 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%//AF062529
- C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%//Q32053
- C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085
- 10 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623
- C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//74aa//45%//P56101
- C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.60E-248//1129bp//99%//AF043733
- 15 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%//AF089814
- C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834
- C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158
- C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//0//2681 bp//99%//AF132022
- 20 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
- C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//2545bp//99%//AB011414
- C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09//169aa//28%//P38074
- 25 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868
- C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516
- C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%//P47943
- 30 C-NT2RP2005767//G.gallus PB1 gene.//5.00E-163//1158bp//81%//X90849
- C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.70E-180//656bp//99%//AF151351
- C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%//Q02038
- 35 C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%//P51005
- C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//0//2191bp//92%//AF155120
- 40 C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39//318aa//31%//P40004
- C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%//P34223
- C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%//AB039669
- 45 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%//P48837
- C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500
- C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%//Q08170
- 50 C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%//AF169797
- C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.10E-214//1026bp//97%//X96484
- C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1669bp//88%//U49055
- 55 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//388aa//32%//P46821
- C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%//AF035262
- C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

- 3.40E-07//50aa//50%//Q61658  
C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.//1.30E-37//484bp//65%//AF055636
- 5 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266  
C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131  
C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966
- 10 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%//P24461  
C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543  
C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538
- 15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973  
C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559  
C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755  
C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%//Q05481
- 20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%//Q62245  
C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//P46401
- 25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692  
C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640  
C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652  
C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
- 30 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%//D29766  
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978  
C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
- 35 C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622  
C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334  
C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
- 40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219  
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293  
C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%//AF061817
- 45 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1.70E-139//679aa//41%//O43143  
C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//319aa//26%//P37908
- 50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066  
C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667  
C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160  
C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%//P15151
- 55 C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%//AF093097  
C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%/P33288  
 C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%/Q07283  
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%/Q13562  
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%/AB012265  
 5 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//5.80E-234//1562bp//81%/AJ251245  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%/P51523  
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%/Q10149  
 10 C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%/P10895  
 C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.00E-10//565aa//24%/P12036  
 15 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%/Q94650  
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%/Q61982  
 C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0//2522bp//99%/AB032470  
 20 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%/P27448  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%/U53445  
 C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138//1673bp//67%/AF227209  
 25 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%/Q03426  
 C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%/P40848  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.70E-185//585bp//88%/AF015264  
 30 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%/P39027  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159  
 C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.80E-38//462bp//70%/AF225902  
 35 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%/Q05481  
 C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.10E-47//537bp//74%/AF060219  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%/AF087433  
 40 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.00E-44//260aa//40%/P55201  
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%/AF097725  
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%/P25386  
 45 C-NT2RP3001120//ZINC FINGER, PROTEIN 136.//7.80E-170//512aa//58%/P52737  
 C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%/P35446  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%/P52154  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.70E-10//196aa//27%/P53154  
 50 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%/P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%/P80193  
 55 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%/P14873  
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%/P32380

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C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.30E-99//669bp//83 %//Y18101

5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508

C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089

10 C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%//AF133913

C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0//1214bp//99%//AJ243467

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

15 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529

C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG.//2.70E-10//159aa//33%//O09053

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P 12270

C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371

20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%//AF205831

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801

25 C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-290//793bp//93%//U63420

C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//345aa//42%//P20964

C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%//Q10022

30 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821

C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0//1730bp//85%//AF163665

C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//2617bp//99%//U35832

35 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609

C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.80E-09//132aa//31%//O22468

C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449

C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0//2836bp//99%//AF149046

40 C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0//2495bp//99%//AB023584

C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1869bp//99%//AF173868

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386

45 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356

C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534

C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%//AF193613

50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177

C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554

C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141

55 C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.40E-15//190aa//32%//Q09701

C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.80E-117//462aa//55%//P52272



- C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.60E-11//348aa//27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652  
 C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.//0//2742bp//99%//AF155135
- 5 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347  
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.//0//1587bp//100%//AB000624
- 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.//4.30E-91//656bp//81%//AF177478  
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458  
 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//3.10E-92//314aa//51%//Q09251
- 15 C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23%//P37709  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//X86779  
 C-NT2RP3002007//SAP1 PROTEIN.//1.1 OE-68//474aa//32%//P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232
- 20 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT.//1.00E-299//397aa//94%//P18484  
 C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374  
 C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3764bp//99%//AF095195
- 25 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//4.10E-233//1896bp//69%//AF111423  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170
- 30 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNBP.//1.90E-151//223aa//91%//Q02614  
 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978  
 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLICISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
- 35 C-NT2RP3002330//Homo sapiens eRF5 mRNA, complete cds.//0//2443bp//99%//U87791  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396  
 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991
- 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792  
 C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45.//8.90E-95//542aa//38%//P38932  
 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010
- 45 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598  
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660
- 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//1703bp//99%//AF111109  
 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%//AF165163  
 C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//97%//AF103731
- 55 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//

41%/P17564  
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%/Q24371  
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%/Q31125  
 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%/P51026  
 5 C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%/AF030430  
 C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%/AF053091  
 C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%/Q13625  
 10 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%/Q04652  
 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%/AF152498  
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%/D89053  
 15 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%/AB029333  
 C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%/AF080158  
 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%/AF084555  
 20 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%/U78090  
 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%/Q02357  
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%/P23645  
 C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%/AB027149  
 25 C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%/D88315  
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%/AB011414  
 30 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%/AF071592  
 C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%/AF077738  
 C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%/P49455  
 35 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%/P52742  
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME 1.//5.70E-09//169aa//31%/Q09674  
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%/AF110267  
 40 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%/U20286  
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%/AB030656  
 C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%/AF098462  
 45 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366aa//48%/P19474  
 C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%/L36983  
 C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%/AB033922  
 50 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%/Q64948  
 C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%/AF117657  
 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.30E-35//178aa//44%/Q62191  
 55 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%/P40084  
 C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%/U09874

- C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
- 5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%//AB019435
- C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
- C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
- 10 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
- C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
- C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 15 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
- C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
- C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
- C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
- 20 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
- C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
- C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
- 25 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
- C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- 30 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
- C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181
- C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- 35 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
- C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
- C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
- 40 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
- C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
- C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
- 45 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
- C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
- C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
- C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
- 50 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
- C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%//AF065391
- 55 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%//AF088982
- C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871
- C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

X67877

- C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.90E-38//462bp//70%//AF225902
- 5 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798
- C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839
- C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820
- C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//42%//P34110
- 10 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%//AB012851
- C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%//U83176
- C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260
- C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484
- 15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%//L11316
- C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%//Q15642
- C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523
- 20 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%//Q01484
- C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0//1853bp//99%//AF040701
- C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922
- 25 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
- C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084
- C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097
- 30 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%//P54352
- C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679
- C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526
- C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375
- 35 C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%//AJ012449
- C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
- C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568
- C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%//AF176667
- 40 C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%//U35776
- C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579
- C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%//P15287
- 45 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
- C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173
- C-NT2RP4000259//GLUTATHIONE PEROXIDASE.2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968
- C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.50E-297//1024aa//55%//P87115
- 50 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.50E-26//237aa//28%//Q01631
- C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%//P26372
- 55 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
- C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%//O75570

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C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738  
C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//  
5 AF221546  
C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-AL-  
PHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701  
C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp//99%//AF083106  
C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309  
C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI-  
10 OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//  
2.50E-37//291aa//38%//P50101  
C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//  
1.90E-67//721aa//29%//Q09475  
C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484  
15 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818  
C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962  
C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755  
C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319  
C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//  
20 99%//AF067730  
C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309  
C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//  
30%//P39625  
C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa//  
25 27%//Q11073  
C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267  
C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524  
C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
0.000000032//67aa//31%//P53915  
30 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSI-  
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640  
C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265  
C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808  
C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-  
35 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175  
C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415  
C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682  
C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314  
C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//  
40 D45913  
C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//  
227aa//36%//Q06828  
C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
45 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//1.50E-76//346aa//43%//Q61068  
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505.//1.40E-07//185aa//25%//Q58900  
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//  
90aa//42%//P38660  
50 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//  
100%//AF094583  
C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579  
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
55 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.70E-16//401aa//26%//P39968  
C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//3.50E-257//  
1377bp//91%//U67140  
C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

AF198487

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%//Q09996

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65//6.70E-51//335aa//37%//Q64375

5 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA<sup>2+</sup>-ATPASE)//1.30E-123//563aa//46%//P13586

C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967

C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//2.30E-07//474aa//22%//P12036

10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1)//2.60E-17//121aa//36%//P51400

C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.90E-115//224aa//100%//P38378

C-NT2RP4001122//MPD PROTEIN//1.40E-65//253aa//41%//O15736

15 C-NT2RP4001126//TRICHOHYALIN//2.90E-18//380aa//26%//Q07283

C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP)//2.10E-07//93aa//33%//P44514

C-NT2RP4001148//SOF1 PROTEIN//1.30E-104//236aa//52%//P33750

20 C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//4.40E-187//731bp//100%//AF037339

C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//3.40E-29//385aa//29%//P35331

C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//4.70E-29//227aa//35%//P52178

25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%//U95760

C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.70E-141//511aa//43%//Q99676

30 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.20E-27//90aa//42%//P38660

C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//1.80E-103//508aa//43%//Q04652

C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene)//0//2006bp//100%//AJ249677

35 C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601

C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082

C-NT2RP4001276//TRICHOHYALIN//7.90E-09//126aa//32%//Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//5.90E-17//296aa//29%//P24391

40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5//8.50E-213//1129bp//92%//AJ001119

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%//O24076

C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein//9.20E-160//736bp//99%//AJ007014

45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%//AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445

50 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.60E-19//222aa//30%//Q08180

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1)//9.20E-17//146aa//35%//P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I//2.00E-53//436aa//30%//Q10085

55 C-NT2RP4001389//KESIPROTEIN//1.70E-31//342aa//34%//P35844

C-NT2RP4001407//TRICHOHYALIN//1.90E-05//298aa//21%//P22793

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//7.70E-190//422aa//82%//Q14141

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.20E-138//419aa//54%//Q99676

- C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds//2.70E-66//738bp//71%//AF129131
- C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE)//0//962aa//78%//Q02218
- 5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1//1.00E-27//374aa//29%//P39010
- C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds//0//2002bp//98%//AF198487
- C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION//5.70E-54//242aa//38%//P25656
- 10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds//0//3202bp//99%//AF152961
- C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-)//4.70E-09//216aa//24%//P96902
- C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN//5.40E-07//213aa//26%//Q02453
- C-NT2RP4001568//ZINC FINGER PROTEIN GCS1//1.80E-10//109aa//36%//P35197
- 15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//0//874aa//96%//P53620
- C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein//0//1087bp//87%//AJ223830
- C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.70E-141//373aa//47%//P73505
- 20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//2.80E-14//652aa//22%//Q02224
- C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19//5.10E-46//234aa//32%//P40469
- C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK)//6.40E-19//111aa//45%//P25323
- 25 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN)//1.10E-45//310aa//27%//P12868
- C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//4.00E-10//243aa//25%//Q10568
- C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//3.00E-10//128aa//32%//Q10282
- 30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//6.40E-170//1168aa//33%//Q09332
- C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//3.90E-236//665aa//58%//P51523
- C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN)//4.10E-16//263aa//27%//P98174
- 35 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds//0//3053bp//99%//AF170025
- C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//1.20E-30//241aa//30%//Q35566
- 40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4//1.10E-19//77aa//54%//P55083
- C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds//6.30E-99//555bp//73%//AF155595
- C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1//1.40E-85//489aa//43%//P55194
- C-NT2RP4001861//HTUCHOHYALIN//1.00E-35//307aa//34%//P37709
- 45 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.40E-08//345aa//25%//Q00808
- C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.30E-38//258aa//32%//Q12024
- C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF//9.80E-60//303aa//38%//P49711
- C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)//1.50E-13//211aa//28%//Q43209
- 50 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//1.20E-13//356aa//27%//P13816
- C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds//0//3203bp//87%//AF195418
- C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds//0//3024bp//99%//AF236056
- 55 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN)//6.90E-24//370aa//27%//Q04652
- C-NT2RP4002047//GTP-BINDING PROTEIN LEPA//1.50E-168//601aa//52%//O67618
- C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.00E-137//679aa//40%//O43143

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C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa//39%//Q05481  
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIAL).//6.70E-06//250aa//31%//P52655  
5 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938  
C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270  
C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552  
C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808  
10 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565  
C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0//2289bp//99%//AF095448  
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116  
15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290  
C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262  
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//O14727  
20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.60E-295//1393bp//97%//AF058922  
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45 %//P80022  
C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957  
25 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761  
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874  
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610  
C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455  
30 C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107  
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.50E-95//461bp//98%//AJ242975  
35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332  
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665  
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904  
40 C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249  
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363  
C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614  
45 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004  
C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205  
C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075  
50 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452  
C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671  
C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850  
C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349  
55 C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0E-310//1440bp//98%//AF121855  
C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-



- plete cds.//0//1812bp//98%//D43772  
 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888  
 C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
 1.10E-209//293aa//95%//P39098  
 5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete  
 cds.//0//759bp//98%//AF038661  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159  
 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//  
 74aa//37%//P49596  
 10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886  
 C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED  
 PROTEIN) (GRP 75).//3.90E-46//78aa//98%//O35501  
 C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199  
 15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584  
 C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484  
 C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440  
 C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%//  
 20 AF132608  
 C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabbp//49%//P32943  
 C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//  
 82%//AB005549  
 25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343  
 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527  
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533  
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978  
 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 30 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566  
 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490  
 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946  
 C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%//  
 AF082657  
 35 C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//2.00E-214//769bp//97%//AJ005897  
 C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//  
 98%//AF167572  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//  
 40 AF051782  
 C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp//  
 93%//AF055008  
 C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//  
 436bp//92%//U94855  
 45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510  
 C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192  
 C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF  
 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568  
 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//  
 50 X62083  
 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//  
 0.0000014//224aa//26%//P25976  
 C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444  
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058  
 55 C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%//AF034801  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp//  
 99%//AJ224819  
 C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

mRNA, complete cds.//0//1715bp//99%//AF135802  
 C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426  
 C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111  
 C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%//  
 5 AB017616  
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
 AF016507  
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
 PROTEIN 1).//0//777aa//91%//P98161  
 10 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081  
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//  
 AF031165  
 C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0//  
 1870bp//99%//AF068302  
 15 C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp//  
 61%//AF133670  
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//  
 38%//Q62267  
 C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
 20 AZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106  
 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796  
 C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%//  
 P08942  
 C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 25 NO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945  
 C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
 0//963bp//99%//U97670  
 C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.70E-190//1624bp//76%//  
 AF068748  
 30 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945  
 C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859  
 C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//  
 0//1083bp//99%//AF203687  
 35 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%//  
 AB029290  
 C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874  
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
 40 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//  
 Q35913  
 C-OVARC100213 8//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955  
 C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213  
 45 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-  
 09//207aa//30%//Q91854  
 C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602  
 C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 50 ZYME).//1.60E-81//212aa//70%//P34547  
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643  
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154  
 C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538  
 C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127  
 55 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.80E-62//158aa//81%//P20290  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//  
 134aa//43%//P52046

C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291  
 C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910  
 C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640  
 5 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246  
 10 C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%//P53368  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245  
 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421  
 15 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455  
 20 C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449  
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201  
 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891  
 25 C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%//AF180371  
 C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043  
 30 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449  
 C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734  
 35 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070  
 40 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742  
 C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278//1476bp//92%//AF110195  
 C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301  
 45 C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
 C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323  
 50 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742  
 C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496  
 C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202//1333bp//80%//D14336  
 55 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652  
 C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds.//6.20E-223//1092bp//78%//AF120207  
 C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

- 99%//AF159567  
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615
- 5 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIREMENT).//3.00E-33//138aa//42%//Q61103  
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//132aa//46%//Q12929  
C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137
- 10 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809  
C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//P51523  
C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408  
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635
- 15 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381  
C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243  
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276
- 20 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290  
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953  
C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159
- 25 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524  
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935  
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908  
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
- 30 C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211  
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.30E-07//188aa//29%//P49606  
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//O76094
- 35 C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679  
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591  
C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505
- 40 C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533  
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233  
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105  
C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274  
C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
- 45 C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273  
C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//U50927  
C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396
- 50 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890  
C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//P39087  
C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
- 55 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.50E-17//76aa//56%//P45340  
C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046  
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

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C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180

C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//9.40E-13//500aa//21%//Q99323

5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%//Q15391

C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201

C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%//U50927

10 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973

C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522

C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//0//1654bp//99%//AB028600

15 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091

C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387

C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321).//1.70E-05//150aa//24%//Q13563

20 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743

C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds.//1.70E-148//687bp//99%//AF182003

25 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//Q15391

C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%//P51522

30 C-PLACE10033537//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715

C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403

C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//AF152463

35 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556

C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475

40 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//7.70E-68//404aa//33%//P32802

C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975

45 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200

C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//Q02516

C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-169//683bp//99%//AF191338

50 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824

C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793

C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8.00E-19//209aa//34%//Q08170

C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282//1316bp//98%//AF053305

55 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742

C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%//AF133423

- C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500
- C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//6.70E-113//501aa//46%//P10895
- 5 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.40E-243//584aa//74%//P17812
- C-PLACE1003915//PROBABLE ARGINYLT-RNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA UGASE) (ARGRS).//2.40E-108//581aa//40%//Q05506
- 10 C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//0//1670bp//99%//AF033120
- C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.40E-124//326aa//73%//P80385
- C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//0//2384bp//86%//AF032666
- 15 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.10E-181//340aa//96%//P29387
- C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds.//3.30E-41//452bp//65%//AF195534
- C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
- C-PLACE1004197//BUTYROPILIN PRECURSOR (BT).//4.50E-10//208aa//27%//Q62556
- 20 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%//AF069493
- C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.//2.00E-93//960bp//76%//AF115778
- C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA.//0//1144bp//98%//AF129112
- 25 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.70E-36//389aa//31%//O15393
- C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//AF084830
- C-PLACE1004302//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750
- C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
- 30 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%//AF100153
- C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.20E-39//385aa//33%//Q63448
- C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
- 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
- C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)7/2.90E-56//276aa//41%//P51522
- C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878
- 40 C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.40E-227//1037bp//99%//AF040701
- C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954
- C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
- 45 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.70E-18//264aa//32%//Q13438
- C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.40E-42//985bp//59%//X66277
- C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.30E-195//982bp//96%//AF035606
- 50 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N- RECOGNIN).//4.40E-35//578aa//27%//O60152
- C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.10E-224//790bp//98%//AB022918
- C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.90E-32//259aa//32%//P30337
- 55 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267
- C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.70E-65//695aa//29%//Q01631

C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170  
 C-PLACE1004868//MALE STERILITY PROTEIN 27//3.90E-39//261aa//27%//Q08891  
 5 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.30E-11//94aa//47%//O42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%//P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%//AF099936  
 C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794  
 10 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa//26%//Q11073  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950  
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652  
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539  
 15 C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577  
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352  
 20 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760  
 C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//O33335  
 25 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251  
 30 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128  
 35 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.10E-148//321aa//83%//P31350  
 40 C-PLACE10057277//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680  
 C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//1.30E-237//585aa//72%//Q60710  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.50E-79//209aa//53%//P08635  
 45 C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//AF027156  
 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 50 C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069  
 C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120  
 C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//1.10E-264//661bp//99%//AF203687  
 55 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE).//5.40E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)/7/1.40E-07//  
 254aa//25%/P38129  
 C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds./2.40E-177//829bp//99%/AF151852  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2./0//1564bp//99%/AJ236876  
 5 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine./4.70E-161//744bp//99%/X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds./1.50E-148//681bp//99%/  
 AF039023  
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
 (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)/2.00E-28//  
 10 236aa//30%/P98110  
 C-PLACE1006167//PAF1 PROTEIN./7.30E-15//437aa//24%/P38351  
 C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT)/1.70E-169//373aa//88%/P17427  
 15 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06./2.70E-116//496aa//48%/Q09747  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN)/2.00E-16//244aa//31%/  
 P28675  
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
 LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM)/4.60E-117//147aa//80%/P21796  
 20 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds./3.00E-07//376bp//59%/U76374  
 C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds./0//1649bp//99%/AF155112  
 C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR)/1.30E-18//460aa//24%/Q00547  
 25 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds./0//1168bp//99%/AF062085  
 C-PLACE1006438//ZINC FINGER PROTEIN 165./2.50E-45//122aa//43%/P49910  
 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME)/1.20E-83//313aa//49%/P27550  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF./7.70E-55//142aa//85%/Q90595  
 30 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)/1.10E-229//367aa//96%/  
 Q00004  
 C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds./0//2618bp//99%/  
 AF137030  
 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds./0//  
 35 2170bp//99%/AF191338  
 C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds./0//1967bp//99%/  
 AF093097  
 C-PLACE1006534//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE,N-ACETYL GALACTOSAM-  
 40 INYLTRANSFERASE) (GALNAC-T1)/8.30E-08//100aa//41%/Q10472  
 C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT)/1.20E-09//426aa//21%/P39922  
 C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds./0//1464bp//99%/U97670  
 C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds./0//1760bp//99%/AB028449  
 45 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328./5.80E-  
 24//734bp//62%/AB015630  
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC  
 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE)/6.90E-13//177aa//33%/Q59263  
 C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN)/6.20E-63//191aa//43%/P13688  
 50 C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG./9.80E-213//232aa//80%/P08547  
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
 TOUS NUCLEAR PROTEIN)/2.00E-15//188aa//29%/P35123  
 55 C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
 NUCLEASE)/1.90E-08//122aa//36%/P16658  
 C-PLACE1006917//HSH49 PROTEIN./5.50E-12//97aa//35%/Q99181  
 C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III./6.70E-48//278aa//41%/



Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30E-86//522aa//36%//P97998

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421

5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542

C-PLACE1007105//Homo sapiens muskellin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489

C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22%//P37709

10 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.50E-216//1068bp//96%//D50495

C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908

15 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.10E-17//1037bp//56%//AF117649

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

20 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007409//WHTTE PROTEIN.//1.10E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487

25 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45%//P08728

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164

30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%//P34537

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506

35 C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa//28%//Q26457

C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535

40 C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602

45 C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415

C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//370aa//25%//Q99323

C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%//P38226

50 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272

55 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

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C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326  
 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//  
 5 31%//Q09531  
 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709  
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
 C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//  
 671aa//77%//P53620  
 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689  
 C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//  
 77%//AF078779  
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-  
 TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315  
 15 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//  
 780bp//100%//AF036144  
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432  
 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED  
 20 PROTEIN) (TAP).//0//698aa//95%//P41541  
 C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%//  
 O42184  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527  
 C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275  
 25 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//  
 48%//P22620  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-  
 CLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN  
 H2).//5.20E-90//483aa//38%//O02668  
 C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8)  
 gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406  
 35 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.30E-269//1225bp//99%//  
 AJ004974  
 C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668  
 C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623  
 40 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
 C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582  
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//  
 30%//P30432  
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814  
 45 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//  
 0//2529bp//99%//AF035586  
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED  
 PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086  
 C-PLACE1009158//Mus musculus mRNA for death inducer-obliteritor-1 (Dio-1).//5.40E-200//1790bp//75%//  
 50 AJ238332  
 C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//  
 1179bp//98%//AF150105  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//  
 55 P34110  
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for  
 mitochondrial product.//2.10E-132//1229bp//75%//AF107295

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%/Q12067  
 C-PLACE1009398//ZINC FINGER PROTEIN 135./6.20E-97//361aa//51%/P52742  
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I./4.70E-08//165aa//33%/Q09820  
 5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds./1.00E-173//1367bp//77%/AF176523  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA)/7.80E-71//82aa//89%/P42356  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)/3.10E-289//550aa//93%/P54319  
 10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III./3.90E-40//179aa//37%/P34580  
 C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds./6.60E-147//592bp//99%/AF043117  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)/7.8.10E-99//228aa//75%/Q99418  
 15 C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds./5.90E-185//857bp//99%/AF078857  
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1./5.10E-54//291aa//40%/Q00808  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN./1.30E-60//209aa//41%/P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)/1.50E-285//538aa//99%/P55161  
 20 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds./0//1854bp//100%/AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I./7.00E-33//166aa//43%/Q09876  
 C-PLACE1009721//MSF1 PROTEIN./1.70E-22//176aa//33%/P35200  
 25 C-PLACE1009731//AIG1 PROTEIN./1.60E-22//274aa//28%/P54120  
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds./4.30E-294//1329bp//100%/AB012190  
 C-PLACE1009798//RLR1 PROTEIN./1.60E-18//270aa//23%/P53552  
 C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)/2.30E-59//405aa//33%/P38968  
 30 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-)/6.50E-28//209aa//38%/P43510  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION./1.90E-108//277aa//43%/P53145  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds./0//1730bp//99%/AF038963  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84)/4.60E-59//450aa//34%/P28175  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds./5.20E-70//736bp//73 %//U48288  
 40 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein./6.00E-279//1402bp//94%/X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./0//2019bp//99%/AF065482  
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)/1.40E-268//506aa//98%/Q62671  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)/7.30E-114//537aa//44%/Q04652  
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3)/1.70E-20//156aa//42%/P22082  
 45 C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I)/4.60E-07//431aa//23%/P35662  
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPUCING COMPONENT, 35 KD) (PR264 PROTEIN)/9.80E-11//95aa//49%/Q01130  
 50 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)/5.1 OE-27//371aa//28%/Q14246  
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN./1.60E-77//214aa//62%/P25722  
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)/1.20E-18//467aa//30%/P46804  
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)/1.10E-09//350aa//22%/P52178  
 55 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)/2.00E-09//126aa//29%/P34024  
 C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds./0//2082bp//91%/AF003927

- C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981 bp//99%//AB022718
- C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%//AF191838
- 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aa//24%//P25386
- C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771
- 10 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546
- C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
- C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
- C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
- 15 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
- C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
- C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
- 20 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267
- C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205
- C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
- 25 C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392
- C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
- C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481
- 30 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
- C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
- 35 C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487
- C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
- C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
- C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894
- 40 C-PLACE1011056//HISTONE HI, GONADAL.//6.80E-13//154aa//37%//P02256
- C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
- C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
- 45 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
- C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
- C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.20E-12//212aa//29%//Q03326
- C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
- C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
- 50 C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265
- C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
- C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
- 55 C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830
- C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695
- C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
- C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

- 4.90E-11//147aa//32%//P52178  
 C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%//L11672
- 5 C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds//4.10E-259//1538bp//87%//AF177476  
 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377  
 C-PLACE1011664//CROOKED NECK PROTEIN.//1.60E-187//505aa//64%//P17886
- 10 C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%//AF095192  
 C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969  
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580
- 15 C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%//AF059617  
 C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%//AF121862  
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.60E-42//104aa//49%//Q09475  
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%//P42566
- 20 C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%//AF082556  
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586
- 25 C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%//P38650  
 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347.//6.30E-166//656bp//94%//AB015629  
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219  
 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
- 30 C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%//Q01082  
 C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%//Q04652  
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098  
 C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0//1554bp//99%//AF069307
- 35 C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205  
 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.60E-16//371aa//28%//P35446  
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//90aa//98%//P10586
- 40 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209  
 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996  
 C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085  
 C-PLACE2000427//PROBABLE HELICASE MOT1.//1.20E-26//200aa//27%//P32333
- 45 C-PLACE2000438//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%//Q10472  
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25//165aa//40%//P33450
- 50 C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//6.70E-127//671bp//94%//AF072733  
 C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAGMENT).//3.50E-30//400aa//30%//P11414  
 C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.//0//2253bp//99%//AF033861
- 55 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267  
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157/1.90E-08//281aa//22%//P22224  
 C-PLACE3000145//TENSIN.//1.00E-108//277aa//75%//Q04205

- C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
- C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
- 5 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020
- C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811
- C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995
- C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
- 10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640
- C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549
- 15 C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290
- C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085
- C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
- 20 C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100
- C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
- C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
- 25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689
- C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabbp//88%//AF091234
- 30 C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481
- C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
- C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
- 35 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
- C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD proteom.//0//5143bp//90%//Z70200
- C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
- C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667
- C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 40 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754
- C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
- C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
- 45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
- C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)7/5.70E-60//254aa//44%//P13002
- C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783
- 50 C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640
- C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
- 55 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//226aa//52%//P10079
- C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//

P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267  
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//  
 431aa//29%//O60100

5 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mito-  
 chondrial protein, complete cds.//0//2384bp//99%//AF047690

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800  
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655

10 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//  
 AB021663

C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709

C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799

15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710  
 C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%//  
 U49055

C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, com-  
 plete cds.//1.10E-159//824bp//95%//U97018

20 C-THYRO1000173//Homo sapiens AP-mu chain family member muB (HSMU1B) mRNA, complete cds.//0//  
 1713bp//99%//AF020797

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//  
 P51523

25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068

C-THY-RO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//  
 99%//AF124145

C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06//  
 280aa//31%//P54259

30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//  
 1325bp//99%//AF072864

C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857

C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085

35 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 4.20E-98//408aa//42%//P19474

C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//  
 AF118566

40 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//  
 AF075587

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//  
 AF140360

45 C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//  
 AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889

C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//  
 3347bp//99%//AF095195

50 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//  
 P98171

C-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-)  
 (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686

C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//  
 2.40E-157//1656bp//70%//U37373

55 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-  
 137//689bp//96%//U62739

C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//  
 2387bp//99%//AF079529

- C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%/P32322
- C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//566aa//37%/P43550
- 5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%/P35132
- C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%/P52491
- 10 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%/P31948
- C-THYRO1001100//ZINC FINGER X-UNKED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%/P98168
- C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%/AF053700
- C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%/AF151835
- C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%/Q05481
- 15 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%/AF136276
- C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%/P45701
- C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%/AF121861
- 20 C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%/AF064729
- C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%/O00154
- C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%/P30427
- 25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%/O70503
- C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%/P35580
- C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%/AJ002190
- 30 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//82%/AF175968
- C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%/AJ225089
- 35 C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa//32%/P45672
- C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%/Q04652
- C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%/P38584
- C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%/P42128
- C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%/AF171060
- 40 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%/AF126484
- C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%/P25916
- C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds.//0//980bp//96%/AF180472
- 45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%/AF132936
- C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp//100%/AF081192
- C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%/AF123534
- 50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%/AF035207
- C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%/Q02910
- C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25%/Q93794
- C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%/AB030835
- C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%/AF157833
- 55 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%/X84692
- C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa//27%/P25343
- C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete



cds.//8.30E-252//1207bp//85%//U41736  
 C-Y79AA1000540//CELL POLARITY PROTEIN TEA1.//2.10E-12//211aa//33%//P87061  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT)7/0//652aa//98%//P17427  
 5 C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.40E-27//216aa//34%//P28320  
 C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//2.00E-287//2031bp//82%//  
 AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942  
 10 C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//0//1594bp//  
 99%//AF093670  
 C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//6.60E-  
 286//1832bp//84%//AF177477  
 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
 15 4.90E-91//200aa//64%//Q61990  
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902  
 C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//1.10E-236//1076bp//99%//  
 AF098799  
 C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds.//  
 20 0//1610bp//99%//AF105369  
 C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//1.60E-284//1288bp//  
 99%//AF072733  
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5.00E-173//220aa//79%//P05209  
 C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17//  
 25 430aa//27%//Q99323  
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete  
 cds.//3.90E-248//1468bp//87%//U38253  
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962  
 30 C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953  
 C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1435bp//  
 99%//AF139658  
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
 35 DROXYSTERIOD DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657  
 C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds.//0//1612bp//99%//AF063015  
 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738  
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//  
 Q03309  
 40 C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.//3.30E-172//1171bp//83%//D87325  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//  
 4708bp//99%//AF055084  
 C-Y79AA1001391//HOMEODOMAIN PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271  
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746  
 45 C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.//8.50E-  
 65//784bp//62%//AF083115  
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132  
 C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//4.50E-193//  
 50 1333bp//80%//D14336  
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
 NASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356  
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.90E-40//482aa//27%//P27550  
 55 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 2.50E-14//410aa//24%//Q00547  
 C-Y79AA1001603//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOS-

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AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537  
 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740  
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//  
 5 227aa//40%//Q01820  
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-  
 47//626bp//68%//AF033120  
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//  
 J04137  
 10 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//  
 0//1689bp//98%//AF177145  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 15 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//  
 AF174602  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 20 SPAC10F6.02C.//1.00E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743  
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329  
 C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357  
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-  
 72//437aa//39%//P00952  
 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//O16264  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620  
 35 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//  
 X67877  
 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725  
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//  
 49%//Q05481  
 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//  
 51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//  
 1444bp//98%//AF129534

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### Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

- 5 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
- 10 3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

- 5     4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
6. A substantially pure protein encoded by polynucleotide of claim 4.
- 10    7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
- 15        (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following  
SEQ ID NOs:

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 SEQ ID NO: 19022, SEQ ID NO: 19024, and SEQ ID NO: 19025

(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence  
 set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:10544, SEQ ID NO:10547, SEQ ID NO:10549, SEQ ID NO:10552, SEQ ID  
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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence  
 selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted,  
 inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino  
 acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the  
 nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equiv-  
 alent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein  
 encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence  
 of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

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- a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
- b) recovering the synthesized product.

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20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

22. A method for detecting the polynucleotide of claim 8, the method comprising:

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- a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
- b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

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23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

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Figure 1

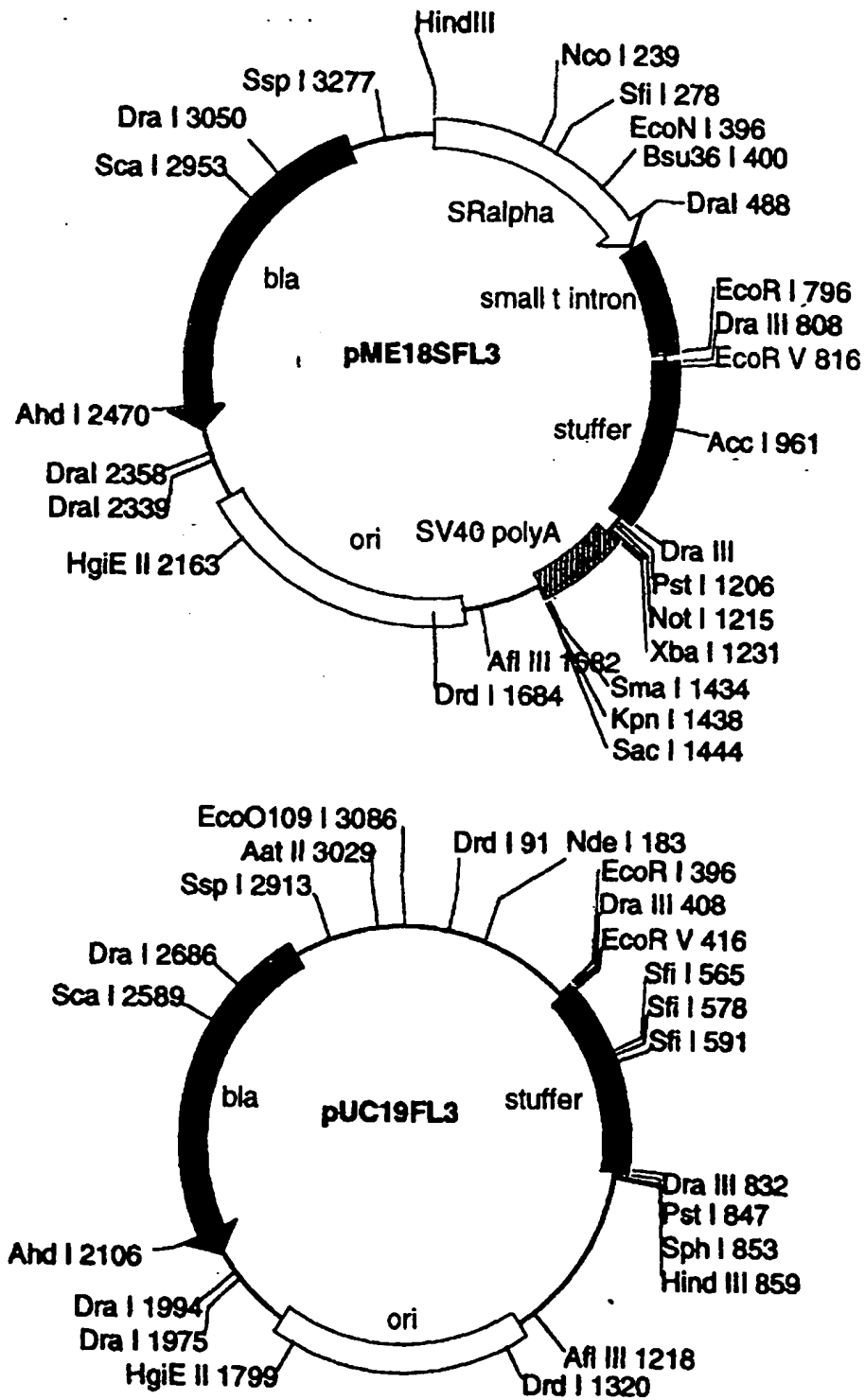


Figure 2

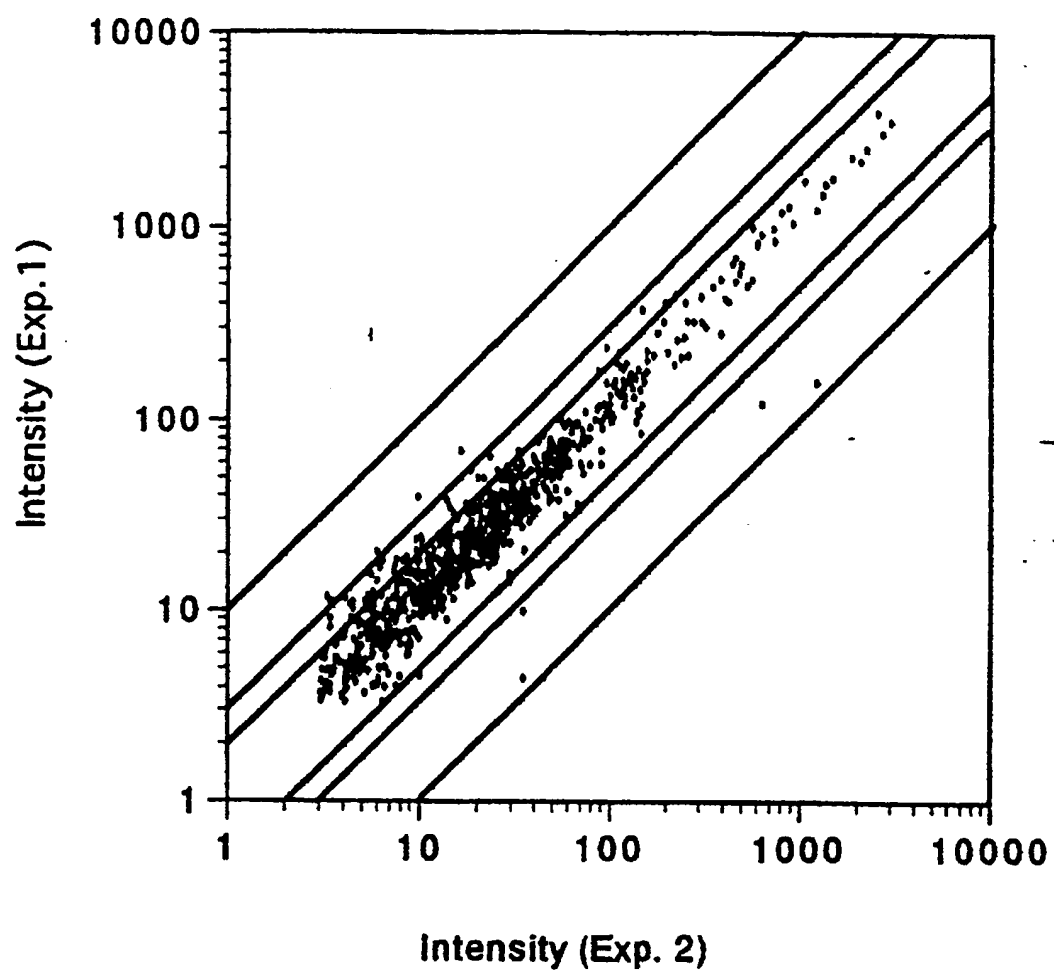


Figure 3

